

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACCGCGTCCGGGCCGGAGCAGCACGGCCGAGGACTGGAGCTCCGGCTCGCTTCCCG
CAGCGCTACCCGCCATGCGCTGCCGCCGGCCGCTGGGCTCCTGCCGCTTCTGCTG
CTGCTGCCGCCGCCGGAGGCCAAGAAAGCCGACGCCCTGCCACCAGGTGCCGGGGCT
GGTGGACAAGTTAACCAAGGGATGGTGACACCGCAAAGAAGAAACTTGGCGGGAAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC
CTGGAGGGCTGTGCGAGAGCAGCAGTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCGACTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGAGATGGGAGCAGACA
GGCGACGGGTCCGCCGGTGCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGGCTGACCAACAGAGACTGCGCGAGTGTGAAGTGGCTGGTGCT
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAAGATGTGGACGAGTGTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACG
AAAATGCTACAATACTCCAGGGAGCTACGTCTGTGTGTCCTGACGGCTTCGAAGAAACG
GAAGATGCCTGTGCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGGAAGACCTGTAATTGTGCCGGACTTACCCCTAAATTATTAGAAGGATGTCC
CGTGGAAAATGTGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGGGGAGAGGCTGC
CTGCTCTCTAACGGTGATTCTCATTGTCCTAAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTTGTATATTTGATACAGTTCTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAGGGCGCCGCACTTGTGTTATTGCAGCTTATAATGGTTACAAATAAGCAATAGCA
TTGGCCGCCATGGCCAACCTGTTATTGCAGCTTATAATGGTTACAAATAAGCAATAGCA
TCACAAATTCAAAATAAGCATTTCAGCTGCATTCTAGTTGTGGTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGAATTAAATTGCCGCAGCACCATGGCTGAAAT
AACCTCTGAAAGAGGAACCTGGTAGGTACCTCTGAGGCGAAAGAACCCAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLPPAPEAAKKPTPCHRGRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESCTKCSGLTNRDCGECEVGWVLDE
GACVDVDECAAEPPPCSAAQFCKNANGSYTCECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDEC SLAEKT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAAC TGCACCTCGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCCGCCAGGCCGGAGGCAGCGGCCAGCGTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGAGTATCTGACGGGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTCCCGCAGCGAGGAGGTCTGAGCAGCAGCATGGCCGGAGGAGCGCCTTC
CCTGCCGCCGCTCTGGCTCTGGAGCATCCTCTGTGCCTGCTGGCACTGCAGGCCGGAGGC
CGGGCCGCCAGGAGGAGGCCTGTACCTATGGATCGATGCTCACCAAGGCAAGAGTACTCA
TAGGATTGAAGAAGATATCCTGATTGTTAGAGGGAAAATGGCACCTTTACACATGAT
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTCAC
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGCTTGCGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGAACAGTGCCTCACAGGCA
TCAGTTGTTCAAGTTGGTTCCCATGTCTGGAAAACAGGATGGGTGGCAGCATTGAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAAATGCTATCT
TCTTAAACATGTCAACAAGCTGAGTGCCCAGGCAGGTGGCATAATGGAGGCTTTGTAAT
GAAAGACGCATCTGCGAGTGTCCCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG
TACCCCACGATGTATGAATGGTGACTTGTGACTCCTGGTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAACTGTGACAAAGCAAACGCTCAACCACCTGCTTAATGGAGGAGC
TGTTCTACCCCTGGAAAATGTATTGCCCTCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCACAACCTGCGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGT
CCAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCAGCCTGGCTGTGGCACAT
GGAACCTGCCATGAACCCAAACAAATGCCATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAAGGTACGAAGCAGCCTCATACTGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC
ACACGCCCTCACTTAAAAGGCCAGGGAGCGGGATCCACCTGAATCCAATTACATCTGG
TGAACCTCGACATCTGAAACGTTTAAGTTACACCAAGTTCATAGCCTTGTAAACCTTCA
TGTGTTGAATGTTCAAATAATGTTCATACACTTAAGAATACTGGCCTGAATTTTATTAGCT
TCATTATAAACTCACTGAGCTGATATTACTCTTCAAGTTCTAAGTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTCTTCTGTTCACTGCTTGGACAGATTTCAGGTTAAATTGGGAAAA
TCAGGTTAAAATTTCAGTGTAGTTGGCAGATATTTCAGGTTAAATTGGGAAAA
GTCTGGGGCAGGGAAACATCAGAAAGGTTAAATTGGGAAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTCACTGCTTATTGTCAAGTATTAGAT
GTTTGTACATTAAAATTGCTCTTAATTAACTCTCAATAACATATAATTGACC
TTACCAATTCCAGAGATTCACTTAAACAAAAAAATTACACTGTGGTAGTGGCATT
AAACAAATATAATTCTAAACACAATGAAATTAGGAATATAATTGTATGAACTTTGCAT
TGGCTTGAAGCAATATAATTGTAACAAAACACAGCTTACCTAATAACATTGAT
ACTGTTGTATGTATAAAATAAGGTGCTGCTTAGTTTTGGAAAAA
AAAAAAAAAAAAAAAGGGCGGCCGCACTTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCAAC TTGTTATTGCAGCTTATAATG

FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNNGFCNERRICECPDGFHGPCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQCRNGGKIGKSCKCSKGYQGDLCSPVVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGGGCGTCCGGCGGTGCAGAGGCCAGGAGGGCGAGGCCGGGGCCAGCCTGGG
CCCCAGCCCACACCTCACCAAGGGCCAGGAGCCACC**ATGT**GGCGATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCGTGGCGCCGG
GAGCTAGCACCGGGTCTGCACCTGCAGGGCATCCGGACGCCGGAGGCCGGTACTGCCAGGA
GCAGGGACCTGTGCTGCCCGCGTGCAGACTGTGCCCTGCCACTCTGGCGCCATCT
GTTACTGTGACCTCTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGGCGTGCCACCCCCCTTTCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA
TCCAGTCTGGGAACGTACTGGACAACGTGAACCGTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTCTGGGGCATGCCCTGGAT**TGAGGGCATTGCTACCGCCTGGGACCA**
TCCGCCATCTCCTCGGTATGAACATGCATGAAATTATAACAGTGCTGAACCCAGGGAG
GTGCTTCCCACAGCCTCGAGGCCTCTGAGAAAGTGGCCAACCTGATTGATGAGCCTCTTGA
CCAAGGCAACTGTGCAAGGCTCTGGGCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCCCTGTCCCTGTGCCCTGAGAACCTGCTGTCTTGAC
ACCCACCAGCAGCAGGGCTGCCCGGGCTCGATGGTGCCTGGTGGTTCTGCGTCTGCGT
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGGCAAGCGCCAGGCCACTGCC
CACTGCCCAACAGCTATGTTAATAACAATGACATCTACAGGTCACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTTCTTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCCCAACTCCTGGGGCC
CAGCCTGGGCGAGAGGGCCACTTCCGCATCGTGCAGGCCGTCAATGAGTGCACATCGAG
AGCTTCGTGCTGGCGTCTGGGCGCTGGGCGATGGGACATGGGTACTCACTGAGGCTG
CGGGCACACGCCGGTCCGGCTGGGATCCAGGCTAAGGGCCGGGAAGAGGCCCAATG
GGCGGTGACCCAGCCTCGCCGACAGAGCCGGCGCAGGCCGGCAGGGCGCTAAT
CCCAGCGGGTTCCGCTGACGCAGGCCCGCTGGGAGGCCGGCAGGGAGACTGGCG
GAGCCCCCAGACCTCCCAGTGGGACGGGGCAGGGCCTGGCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCCTGGCGCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCCACCCCAATCCGTATTCTTTTTTTTTAGACAGGGTCTGCTCCG
TTGCCAGGTTGGAGTGCAGTGGCCATCAGGCTCACTGTAACCTCCGACTCCTGGTTCA
AGTACCCCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCAACACCTGGC
TAATTTGTATTTGTAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAAC
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCTCCAAAGTGTGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTCACTGTTAAAAA
TAAAACCAAAGTATTGATAAAAAAAA

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYEQDLCCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPIQGCMHGGRIYPVLGYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG
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N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTTGGCCCTTTCCACAGCAAGCTNTGCNATCCCGATTCGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCCTGTCCTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCGCTGGTGGTTCCCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGGCAAGGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGTCTACCGCCTGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGGCCCTATGGAGG
TGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGATGCAGGTGGAGAATGCACCCAGCTGGGG
GAGCAGTGCTGGACCCCGCGCATCCGCGCAGTGGCCTCCTGACCGTAT CAGCAAAGGCTG
CAGCTGAATGCGTGGAT GACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCCAGGGGGCCCATGCCCTGCAGCCGGCTGCCCATCCTT
GCGCTGCTCCCTGCACTCGGCCCTGCTGCTTGGGGACCCGGCCAGCTATAGGGCTTGGGGGG
CCCCGCTGCAGCCACACTGGGTGTGGTCCCCAGGCCTTGTGCCACTCCTCACAGACCT
GCCCAGTGGGAGCCTGTCCTGGTCTGAGGCACATCCTAACGCAAGTCTGACCATGTTATGT
CTGCACCCCGTCCCCACCCCTGACCCCTCCATGGCCCTTCCAGGACTCCACCCGGCAGA
TCAGCTTAGTGACACAGATCGGCTGCAGATGGCCCTCCAACCCTTCTGCTGCTTTC
CATGGCCAGCATTTCCACCCTTAACCCGTGCTCAGGCACCTCTCCCCCCAGGAAGCTT
CCTGGCCACCCATTATGACTTGAGCCAGGTCTGGCCGTGGGTCCCCCGACCCAGCA
GGGGAAGGCACTCAGGAGGGCCCAGTAAAGGTGAGATGAAGGTGGACTGAAGTGAACTGGA
GGACAAAGAGGTCGACGTGAGTTCCTGGAGGTTCCAGAGATGGGGCTGGAGGGCTGGAGGGA
GGGGCAGGCCTCACATCGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGGCCTT
AATAAAAACCCTGTGGATAAGCCAAAAAA

FIGURE 9

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSLDT
DPPADGPSNPLCCCFHGPAFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCACCGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGCGCAGATCCGCAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTCAGGTCAACGGCGTCGCATCTCCGCCACGCCAGGGCAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGAAGAGCAAAGACTG
CGTGTTCACGGAGATCGTGGAGAACAACTATAACGCCCTCCAGAACGCCGGCACGAGG
GCTGGTTCATGGCCTTCACGCCAGGGCGGCCAGGCTTCCGCAGCCGCCAGAAC
CAGCGCGAGGCCACTTCATCAAGCGCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC
CGAGAACAGCAGTCAGTTGAGTTGTGGCTCCGCCAACCGCCGGACCAAGCGCACAC
GGCGGCCCAAGCCCTCACGTAGTCTGGAGGCAGGGGCAGCAGCCCTGGCCGCCTCCC
CACCCCTTCCCTTCTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCCCTGAGGGCCCGAAGCATCCGAGCCCCCAGCTGGGAAGGGCAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTGCCCTTCCGGACGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTCAACCTGATCTCAGGCCACCAGCCTGCGCCCTCCAGCCGGCTCCTGAAGCC
CGCTGAAAGGTCAAGCGACTGAAGGCCCTGCAGACAACCGTCTGGAGGTGGCTGTCCCTAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGGCCCCAAACTCCTCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTGTTCAAGAAAAAAAGAAAGGGAGAGAGAGGAAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCACTCCCAGCCC
CGGAATAAAACCATTTCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGSKDCVFTEIVLE
NNYTAFQNARHEGWFMADFTRQGRPROASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

 **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

 **Casein kinase II phosphorylation site.**

amino acids 65-69

 **Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

 **N-myristoylation site.**

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAATTCTCCCTGTTGAATTTTGACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCACATCCAGT
CATTGGATTGCTGTTATTTTTCTTTCTTTCCCACCAATTGTATTTAT
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGCTTTCT
GAAGTCTTGGCTTATCATTCCTGGGCTCTACTCACAGGTGTCACAGGCTTCCATTGACCTCAGT
CTAGTGTGCCGCTCGACAGGAACCTGTACTGTAATGAGCGAAGCTTGACCTCAGT
CCTCTGGGATCCGGAGGGCGTAACCGTACTCTACCTCCACAAACAACCAAATTAAATAATGC
TGGATTCCTGCAGAACTGCACAATGTACAGTCGGTGACACGGCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTCCAAGAACATGTACAGGTTCTCCATTGCAGGAAAC
AATATTGAGACCATTTCACGGGCTGCTTGCCTGAGCTTGAAGCTTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCCTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGCTTCCGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAATCGAATTGCTGTATATCCGACATGGCCTCCAGAA
TCTCACGAGCTTGGAGCGTCTATTGTGGACGGAACCTCCTGACCAACAAAGGGTATGCCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTACGTAATTGCTGTCC
CACCCCTCCTCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAGGACAACCAAGAT
~~AAACACATTCTTGACAGCCTCTCAAATCTCGTAAGCTGGAACGGCTGGATATATCCA~~
~~ACAACCAACTCGGGATGCTGACTCAAGGGTTTTGATAATCTCTCCAAACCTGAAGCAGCTC~~
~~ACTGCTCGGAATAACCCCTGGTTTGTGACTGCAGTATTAAATGGGTCAAGAACATGGCTCAA~~
~~ATATATCCCTCATCTCAACGTGCGGGGTTCATGTGCCAAGGTCTGAACAAGTCCGGG~~
~~GGATGGCCGTAGGGAAATTAAATGAATCTTGTCCCTGACCACGACCCCCGGCCTG~~
~~CCTCTTCAACCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCACCCCTCTAT~~
~~TCCAAACCTAGCAGAAGCTACACGCCTCAACTCCTACCACATCGAAACTTCCCACGATT~~
~~TCTGACTGGATGGCAGAGAAAGAGTGAACCCCACCTATTCTGAACGGATCCAGCTCTATC~~
~~CATTTGTGAATGATACTTCAAGTCAGCTGGCTCTCTCTTCAACCGTGTGGATA~~
~~CAAACTCACATGGGTGAAATGGGCCACAGTTAGTAGGGGCATCGTCAGGAGCGCATAG~~
~~TCAGCGGTGAGAACACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT~~
~~TGTTAGTGCACGGATGCTTTAACTACCGCGCGTAGAAGACACCATTGTTAGAGGC~~
~~CACCAACCCATGCCTCTATCTGAACACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA~~
~~CGTCCCACAGCATGGCTCCCCCTTCTGCTGGGGCTTGATGGGGGGCGCGGTGATATT~~
~~GTGCTGGTGGCTTGCTCAGCGTCTTGCTGGCATATGCACAAAAGGGCGCTACACCTC~~
~~CCAGAAGTGGAAATACAACCGGGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA~~
~~AGGACAACCTCCATCCTGGAGATGACAGAAACCAAGTTTCAGATCGTCTCCTAAATAACGAT~~
~~CAACTCCTAAAGGAGATTCAAGACTGCAGCCATTACACCCAAATGGGGCATTAAATTA~~
~~CACAGACTGCCATATCCCCAACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC~~
~~ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCAGAACATTAGACTCTTGAGAA~~
~~CACACTCGTGTGTCACATAAAGACACGCAGATTACATTGATAATGTTACACAGATGCAT~~
~~TTGTGCATTGAATACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAGTG~~
~~CTATCTTCTATTCAAGTTAATTACAAACAGTTGTAACTCTTGCTTTAAATCTT~~

FIGURE 13

MGLQTTKWPShGAFFLKS~~W~~LI ISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGTVLVLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNRVLHLQENNIQTI
SRAALAQLLKLEELHLD~~D~~NSISTVGVEDGAFREAISLKLFLSKNHLSVPVGLPVDLQELR
VDENRIAVisDMAFQNLTS~~L~~ERLIVDGNLLTMKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMAR~~E~~LN~~M~~NLLSCPTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPPTT~~S~~KLPTIPDWDGRERVT~~P~~PISERIQLSIHFVND
TSIQVSWL~~S~~FTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLUVL
LSVFCWHMHKKGRYTSQWKYNRGRRKDDYCEAGTKKD~~N~~SILEMTETSFQIVSLNN~~D~~QLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

 **N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

 **Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

 **Tyrosine kinase phosphorylation site.**

amino acids 319-328

 **N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,

522-528, 545-551, 633-639

 **Amidation site.**

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTGGAGCAAGCGCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGCTCCGTCCGCCTCCCACGAGCG
ATCCCGAGGAAGCCGGCCCTCGCGAGCGAAGAGGCCGACGGAGGAAGACCCGGGTGGCTGCGCCCTGCC
TCGCTTCCCAGCGCCGGCTGCAGCCTTGCTCCCTTGAAATGGAAAAGATGCTCGCAGGCT
GCTTCTGCTGATCCTCGACAGATCGTCCCTCCCTGCCAGGGCAGGGAGCGGTACGTGGAGGTCCATCT
CTAGGGCAGACAGCTCGAACCCCGCAGACGGCCCTCTGGAGAGTTCTGTGAGAACACAAGCGGGCAGACC
TGGTTTCATCATGACAGCTCTCGCAGTGTCAAACACCCATGACTATGCAAAGGTCAAGGGAGTTCATGTGGACA
TCTTGCATTCTGGACATTGGTCTGTGACAGTGTGACCCAGTGGGCTGCTCCAATATGGCAGCACTGTCAAGAATG
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGAGCGTGTCAAGAGGATGCGGCATCTGTCCACCG
GCACCATGACTGGCTGGCATCCAGTATGCCCTGAAACATCGCATTCTCAGAACAGGAGGGGGCCCCGGCCCTGA
GGGAGAATGTGCCACGGTCATAATGATCGTACAGATGGAGACCTCAGGACTCCGTGGCCAGGTGGCTGCTA
AGGCACGGGACACGGGCATCCTAATCTTGCCATTGGTGTGGCCAGGTAGACTCAACACCTTGAAGTCCATTG
GGAGTGAGCCCCATGAGGACCATGTCCTGTGGCAATTCAAGCCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGACGGCCACATGTGCAGCACCTGGAGCATACTGTGCCACTCTGCATCAACATCCCTG
GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACACTTGAGAATCCAGGATCTGT
GTGCCATGGAGGACACAACGTGAGCAGCTGTGTGAATGTGCCGGCTCTCGTGTGCAAGTGTACAGTG
GCTACGCCCTGGCTGAGGATGGAAAGAGGTGTTGGACTACTGTGCCCTGAGAAAACCACGGATGTGAAC
ATGAGTGTGAAATGCTGATGGCTCTACCTTGCCAGTGCATGAAGGATTGCTCTTAACCCAGATGAAAAAA
CGTGACAAGGATCAACTACTGTGACTGAACAAACCGGGCTGTGAGCATGAGTGCCTAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCAAATGGAAAACCTGCAGCCAGTGGACCACTGTGCAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTGAACACGGAGGATTCTCGTGTGCCAGTGCTCAGAAGGCTTCC
TCATCAACGAGGACCTCAAGACCTGCTCCGGTGGATTACTGCCCTGCTGAGTGACCATGGTTGTGAATACTCCT
GTGTCACATGGACAGATCCTTGCTGTCAGTGTCTGAGGGACACGTGCTCCGCAGCGATGGAAAGACGTGTG
CAAATGGACTCTTGTGCTCTGGGGACCACGGTTGTGAACATTGTGTGAAGCAGTGAAGATTGTTGTG
GCCAGTGCTTGAAGGTTATTAACACTCCGTGAAGATGGAAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTATAG
ACCATGGCTGTGAACACATTGTGTGAACAGTGCAGACTCATACACGTGCGAGTGTGCTGGAGGGATTCCGGCTCG
CTGAGGATGGGAAACGCTGCCGAAGGAGGTGCTGCAAATCAACCCACATGGCTGCCAACACATTGTGTTA
ATAATGGGAATTCTACATCTGCAAATGCTCAGAGGGATTGTTCTAGGTGAGGACGGAAAGACGGTCAAGAAAT
GCACGTGAAGGCCAATTGACCTGGTTGTGATGGATCCAAGAGTCTGGAGAAAGAGAATTGAGGTG
TGAAGCAGTTGTCACTGAAATTATAGATTCTTGCAAACTTCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGT
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTCAACTGCCAACAGACATGAAAAAAGCCGTGGCCC
ACATGAAATACATGGGAAAGGGCTTATGACTGGCTGCCCTGAAACACATGTTGAGAGAAGTTTACCCAAG
GAGAAGGGGCCAGGCCCTTCCACAAGGGTGCCAGAGCAGCCATTGTGTTCACCGACGGACGGCTCAGGATG
ACGTCCTGGAGGGCCAGTAAAGCCAAGGCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAGCCATTG
AGGAGGAACATACAAGAGATTGCCCTGAGCCCACAAACAAGCATCTTCTATGCCAACAGACTCAGCACAATGG
ATGAGATAAGTAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAACAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGGAACTGCCAAAACGGTCAACAGCCAACAGAACATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT
CCTGTTCTAATTGCAAGTGCACACAGATATCTGTTGAAGAAGACAATCTTACGGTCTACACAAAGCTTT
CCCATTCAACAAACCTCAGGAAGCCCTTGAAGAAAACAGCATCAATGCAAATGTGAAAACCTTATAATGT
TCCAGAACCTTGCAAACGAAGAAGTAAGAAAATTAAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGGCC
TGGAAAATGCCCTGAGATAACAGATGAAGATTAGAAATCGCAGCACATTGAGTCATTGTATCACGGATTACAAT
GAACGCAGTGCAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGAGTAAAACAATCAGTACTGA
GAAACCTGGTTGCCACAGAACAAAGACAAGAAGTATACTACTAACTGTATAAATTATCTAGGAAAAAAATCCT
TCAGAATTCTAAGATGAATTACCAAGGTGAGAATGAATAAGCTATGCAAGGTATTGTTGAAATATACTGTGGACAC
AACTTGCTTCTGCCCTACCTGCCTAGTGTGCAATCTCATTGACTATACGATAAAAGTTGCACAGTCTTACTT
CTGTAGAACACTGGCCATAGGAAATGCTGTTTTGTACTGGACTTACCTTGATATGTATGGATGTATG
CATAAAATCATAGGACATATGTACTTGGAACAAGTTGGATTTTATAACATATAAAATTCCACACTTCAG

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGRHARTHPOQTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFRKSEVERAV
KMRHLSTGTMGLAIQYALNIAFSEAE GARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIGVGVQDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKGPC
EHECVNMEESYYCRCRGYTLDPNGKTCSRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSRGKTCAKLDSCALGDHGCE
HSCVSSEDSFVCQCFCFGYILREDGKTCCRKDVCQAIDHGCEHI CVNSDDSYTCECLEGFR LA
EDGKRCRRKDVKSTHHGCEHI CVNNNGNSYICKCSEG FVLAEDGRRCKCTEGPIDLVFVID
GSKSLGEENFEVVVKQFVTGIIDS LTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHM FERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEALESDGRQDS
PAGELPKTVQOPTESEPVTINI QDLLSCSNFAVQHRYLFEE DNL LRSTQKLSHSTKPSGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCGCGCACGCTCCGCCGCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCGCGCTGGCGCCCTGACTCCGTCCGCCAGGGAGGGC
CATGATTCCCTCCCAGGGCCCTGGTGACCAACTTGCTGCGTTTTGTTCTGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCAC TTGCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACACTTGCACGGGAGGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTGATGTGGTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCATACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATAAAACCT
TAGAACTCAATGTACTGGTCCCTCCAGCTCCTCCATCCTGCCGTCTCAGGGTGTGGCCCAT
GTGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTCCAGACTTCTTGACCCAGCATTAGATGTCATCCGTG
GGTCTTAAGCCTACCAACCTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGGTACCCCTGGTGGACTGGGGTGTGGCTGGCTGGTCC
TCTTGTACCACCGCCGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCTGCCCTGGCCAAGAGCTCAGACACAATCTCAAGAATGGGACCC
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCATGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGAT
GGGGCCCACCCCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCCTGCCAGAGTCAGCTGGCTCTGGTAT**GATGAC**
CCCACCACTATTGGCTAAAGGATTGGGTCTCTCCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCAACCTCTC
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGAGGAGCCTCCACCCACCCCTGACTCCTCCTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTGAGTCTCCAGGC
CCCCCTGATCTGTACCCACCCATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAAGCTGGCTGGTTAGGTTTACTGGGCAGAGGATAGGAAATCTC
TTATTAAAACATGAAATATGTGTTTTCAATTGCAAATTAAAGATACTAA
TGTGTTGATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLP AWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNL SLRLEG LQEKD SG PY
SCSVNVQDKQGKS RGH SIKTLELNVLVPPAPPSCRLQGVPHVG ANVTLSC QSPRS KPAVQY Q
WDRQLPSFQTFFAPALD VIRGSLSLTNLSSMAGVYVCKAHNEV GTAQC NVTLEVST GPGAA
VVAGAVVGTILVGLGLLAGLVLLYHRRGKALEEPANDI KEDAIA PRTL PWPKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR
MGAVPVMVPAQS QAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTCGGGCACCGCCA**ATGAAACGCCTCCGCTCTAGGGTTTCCACTTG**
TTGAATTGTCCTATACTCAAAATTGCCACCAAGACACCTGTCTCCAAATGAAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAAGGAAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGAAATTAACTCAGCCTGTGGCAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTCAGATCCAGCAGTAACCA
AGACAGGTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGCCATT
TAGATAATGTCTGTATAGCTGCAAATTAAATAAAAACCTTAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAGAAATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAAACA
CTATCTCAGCCAAGGACACCCCTTCTAACTCAACTCTTACTGAATTGTAACAAACCGTGAAT
AATTGTTCAAAGGGATACATTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTGATAACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTGAT
TCATATAACATGAAACATATTCACTCCTCATATGAATATGGATGGAGACTACATAAATATA
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTCATTTATA
AGAGTATTGGCTTGTGTTCATCATCTGACAACCTTCTTATTGAAACCTCAAATTATGAT
AATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTAAACCC
ACCCACATTATATGAACATTGAAAAAAACATTACATTAAAGTCATCGAAAGGTACAGATA
GGTATAGGAGTCTATGTGCATTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTGCAATTGATGTCCTCTGGCCTTCATTGGTATTAAAGATTATAATATTC
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGCTTGCATATGCATTTC
ACCTCTGGTCTTCAGTGAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTGCTG
TAGCCTATTCTTGCTGAACTGTTCTTCTGTTGGATCAATACAAATACTAATAAGCTCT
TCTGTTCAATCATTGCCGACTGCTACACTACTCTTTAGCTGCTTGCATGGATGTGC
ATTGAAGGCATACATCTCATCTCATGTTGGGTGTCATCTACAACAAGGGATTGGCA
CAAGAATTTCATCTTGCTATCTAACGCCAGCCGTGGTAGTTGGATTTCGGCAGCAC
TAGGATAACAGATATTATGGACAAACAAAGTATGTTGGCTTAGCACCGAAAACAACATTATT
TGGAGTTTATAGGACCATGCCTAACATTCTGTTAACATCTCTGGCTTGGAGTCAT
CATATACAAAGTTTCGTACACTGCAGGGTGAAACCAGAAGTTAGTGTCTTGAGAACAA
TAAGGTCTTGTGCAAGAGGAGCCCTCGCTCTCTGTTCTCGGCACCACCTGGATCTT
GGGGTTCTCCATGTTGTGCACGCATCAGGGTACAGCTTACCTCTCACAGTCAGCAATGC
TTTCCAGGGATGTTCATTTTATTCTGTGTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTTCAAAATGCCCCGTGTTGGATGTTAAGG**TAAACATAGAGAATG**
GTGGATAATTACAAC TGCAACAAAATAAAATTCAAGCTGTGGATGACCAATGTATAAAA
TGACTCATCAAATTCCAATTATTAACACTAGACAAAAGTATTAAATCAGTTTCT
GTTTATGCTATAGGAAC TGAGATAATAAGGAAAATTATGTATCATATAGATATACTATGT
TTTCTATGTGAAATAGTTCTGTCAAAATAGTATTGCAAGATATTGGAAAGTAATTGGTT
CTCAGGAGTGTATCACTGCACCCAGGAAAGATTCTTCTAACACAGAGAAGTATATGAA
TGTCTGAAGGAAACCACTGGCTTGATATTCTGTGACTCGTGTGCTTGAAACTAGTCC
CCTACCACCTCGGTATGAGCTCATTACAGAAAGTGGAACATAAGAGAATGAAGGGGCAGA
ATATCAAACAGTGAAAAGGAATGATAAGATGTATTGAAATGAACTGTTTCTGTAGAC
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAGAACACATTACCTTACCTTGTGAA
TTGTTCTGAACCTAAATGTCCACTAAAACAACCTAGACTCTGTTGCTAAATCTGTTCTT
TTCTAATATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLLVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENVANCHLDNV CIAA
NINKTLTKIRSIKEPVALLQEYRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL
SNSTLTFEVKTVNNFVQRDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSFKTTEFDT
NSTDIALKVFVFFDSYNMKHIHPHMNMDGDYINIIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLKPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDYRSLCAF
WNYSPDTMNGWSSEGCELYSNETHTSCRNCNLTHFAILMSSGPSIGIKDYNILTRITQLG
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFC SIIAGL
LHYFFLAFAWM CIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPA VVVGFS AALGYRYYGT
TKVCWLSTENNFI WSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVVLHV VHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKI QEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTGCATTTATATTATAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAATAAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTTGGAATACTCACCTGATACCAGTGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTTACCTTC
TGGTTCTCAGTGAATTCAAAGCACCAAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGTGGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCTCCGCAGATCCGAACGGCTGGCGGGGTCAACCCGGCTGGGA
CAAGAAGCCGCCGCTGCGCTGCCGGGCCCAGGGGGCTGGGGCTGGGGCTGGGGCCGGAGGC
GGTGTGAGTGGGTGTGTGCGGGGGCGGGAGGCTTGATGCAATCCGATAAGAAAATGCTCGGG
TGTCTTGGGCACCTACCGTGGGCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG
CCGCCGCGCCGTCAGAGCAGGAGCGCTGCCTCAGGATCTAGGGCACGACCATCCAACCC
GGCACTCACAGCCCCGAGCGCATCCGGTCGCCAGCCTCCGCACCCCCATGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCGTGGCCGGCGCCCCCTGCCCTCTGGACGCCGGGCC
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCCGACCTGTACACCTCCGGCCCC
ACGGGCTCTCCAGCTGCTTCTGCCATCCGTGCCAGGGCGTGTGGACTGCCGCCGG
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTCTGCCGACCGTGGCCATCAAGGG
CGTGCACAGCGTGCCTGACCTCTGCATGGGCCCGACGGCAAGATGCAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAACGCCCTCCGGCTCCCTGAGCAGTGCCAAACAGCGGAGCTGTACAAGAA
CAGAGGTTTCTTCACTCTCTCATTCCCTGCCATGCTGCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG
GACCCATTGGCTTGTACCCGACTGGAGGCCGTGAGGAGTCCAGCTTGAGAAGTAA
GAGACCATGCCGGCCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGACG
TGCTTCTACAAGAACAGTCTGAGTCCACGTTCTGTTAGCTTAGGAAGAACATCTAGAA
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCCAGTTCTAGCCAATAGACTGTCTGAT
CATAACATTGTAAGCCTGTAGCTTGCCTGCCAGCTGCCCTGGGCCCTATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGCTCAGTTCTGCTGAATAACCTCCATCGATGGGGAAC
TCACTTCCTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTCATCACTTC
CCCAGGAGCAGCCAGAACAGCAGGAGTAGTTTAATTCAAGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAAATTCACTCAACCCATGTGGAATTGATCTATCTACTTCCAGGG
ACCATTGCCCTCCAAATCCCTCCAGGCCAGAACACTGACTGGAGCAGGCATGGCCACCA
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAATTGAGAATTCCCC
CTGAGGCCAGTTCTGTCATGGATGCTGCCGTGAGAATAACTGCTGTCCGGTGTACCTGC
TTCCATCTCCAGCCCCACCGAGCCCTGCCACCTCACATGCCCTCCCATGGATTGGGGCCT
CCCAGGCCCCACCTTATGTCAACCTGCACTTCTGTTCAAAATCAGAAAAGAGAT
TTGAAGACCCAAGTCTGTCAATAACTGCTGTGTGGAAGCAGCGGGGGAGACCTAGAAC
CCTTCCCCAGCACTGGTTCCAACATGATATTATGAGTAATTATTTGATATGTACA
TCTCTTATTCTACATTATTATGCCCAAATTATATTATGTATGTAAGTGAGGTTG
TTTGTATATTAAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGACCCCTGACCTCCTCA
GAGCAGCCGGCTGCCGCCGGAAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTGCTG
CTGCTGCCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGGTTTCTGCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCAA
AGAAGACTTTCCAGATTAGAGTGGAGAAACTGGGTGGAGTGTCTCCTTGTCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAATGTGACAAGAAGTGTGAGCTGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAACCTGGAAGAGGATAACAGTCACTCTGGAAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGAATCCAGCTCCTGAATAACACATGGTTAAGGATGGCATCCGTTGCTAGAAA
ATCCCAGACTTGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAAAACTGGAAC
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCCCTGTGAAGCCCGCAATT
TGTTGGATATCGCAGGTGTCCCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTAGTGATTCCTGTGGCTTGTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTGGAAAGG
CCGGCGGGCGGATCACGAGGTCAAGGAGTTCAGACCAGTCTGGCCAATATGGTAAACCC
CATCTCTACTAAAATACAAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTGAACCCGGAGGCAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAATAAAATAAAATA
AATAAAATCTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDDQQVVTAVEYQEAILACKTPKTVSSRLE
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGI
LLLENPRLGSQST
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNVGYRRCPGKRMQVDDLNI
SGIAAVVVVA
LVISVCGLGVCYAQRKGYSKETSFQKSNSSSKATTMSENVQWLTPV
IPALWKA
AAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATTAACATGCTCACAGCCGGACCCCTGGCAT
CATGCTGCTATTCTGCAAATACTGAAGAACATGGGATTAAATATTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCACATCTACATACATACTCCACCTCAAAAAGTACATCAATA
TTATATCATTAAAGGAATAGTAACCTCTTCTCCAATATGCATGACATTGGACAATG
CAATTGTGGCACTGGCACTTATTCAGTGAAGAAAAACTTGTGGTTCTATGGCATTCATCA
TTTGACAAATGCAAGCATCTCCTTATCAATCAGCTCTATTGAACTTACTAGCACTGACTG
TGGAATCCTTAAGGGCCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCTATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACCTCCAGCCAGATTGCC
AGCTAACACACAGATTCTCTACAGACTAACAAATTGCAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTACTGGCCTGGATTATCTCAAAACAATTATCAGTCACCAAT
ATTAATGTAAGGAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAACAAACTACTGA
ACTGCCTGAAAATGTCGCACTGAGCAACTACAAGAACTCTATATTAAATCACAACT
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTTCTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTTCAAATCTAGAGAT
TCTGATGATTGGGAAAATCCAATTATCAGAACATGAACTTTAACCTCTTATCA
ATCTTCGAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCCTGGTT
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCCATGT
TGCTCTTCAAAGTGTAAATCTCAAATTGGATCTAAATTAAATCTTATTAGAA
TACGAAGGGGTGATTTAGCAATATGCTACACTAAAAGAGTTGGGGATAAAATAATATGCCT
GAGCTGATTCCATCGATAGTCTGCTGTGGATAACCTGCCAGATTAAAGAAAATAGAAGC
TACTAACACCCCTAGATTGTCTTACATTCAACCCCAATGCATTTCAGACTCCCCAAGCTGG
AATCACTCATGCTAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCATGGTACTCTG
CCAAACCTCAAGGAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTCATCCGTG
GATGAACATGAACAAAACCAACATTGGATTCTGGAGCCAGATTCACTGTTTGCCTGGACC
CACCTGAATTCCAAGGTCAAATGTTGGCAAGTGCATTTCAGGGACATGATGGAAATTG
CTCCCTCTTATAGCTCTGAGAGCTTCTTCTAAATCTAAATGAGAGCTGGGAGCTATGT
TTCCTTCAGTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTCTG
GTCAAAACTCTGCCTAATACCCCTGACAGACAAGTTCTATGTCCTATTGAGGGAAACACTA
GATATAATGGCGTAACTCCCCAAGAAGGGGTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTGAAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAAATG
GCTCTTGAATATTAAAATAAGAGATATTCAAGGCCATTCAAGTTGGTGTCTGGAAAGCA
AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA
TGCTGCGCAAAGTGCCTGAATACCACATGTATGTCAGGTATATACTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTACAGAAAAACAGAAAAAAA
TGTGTAATGTCACCACCAAGGTTGCACCCCTGATCAAAAAGAGTATGAAAAGAATAATAC
CACACACCTATGGCCTGTCTGGAGGCCTCTGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCCTCTCCAGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG
AAACCAACCTTGCAATTAGGTGAGCTTATCCTCTGTATAAATCTCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTCT
AAAAACCACCAAGGAAACCTACTCCAAAAATGAAC

FIGURE 26

MKDMPPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNIAKIEYSTDYPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLRLHLSNRQLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSVIAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVNLKFLLDNKNPINRIRRGGDFSNMLHLKELGINNMPELISIDSLAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSAHYHTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEPDSDLFCVDPPFQGQNVROVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRAAEQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLINGVTPKEGGLYTC
IATNLVGAIDLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTLMACLGGLGIIGVICLISCLSPEMNCDGGHSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGTGGAGTAGATGAGGAATGGCTCGTATTATGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCGTTCCCTCCATGTGTCTCCTCCTACAAAGTTGTTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTGTCTCCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTTCTAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAATGCCTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACACCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTGGCTGGTCACTATGGTGTCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG
GATGCCCGAGACACCTCGAATACTTGAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTGCAGTGCAGTAGAAATAAGTGGTTACTTCTCCATCCATTGTAAACATTGAA
ACTTGTATTCAGTTTTTGAAATTATGCCACTGCTGAACCTTAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTTT
AATTAAAAGCAAATAAAGCTTAACTTGAACCAGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMC PKGCLCSSGGLNVTCSNANLKEIPRDL
PPETVLLYLDNSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR
IQSVHKNAFFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFL
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGAACGAAGGCAGCAGGGATGCAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCTGGCCTGCTGGCAGCCCACCTCTGCTGGTGC
GGGCTCAGTGTGTCAGGCTCGGCCACGGCTGCCCGCCGCTGCGAGTGCTCCGCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTAACCGAGCAGGACGAGTTGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGGCCGGCG
CCTTCAACAACCTCTCAACCTCCGGACGCTGGTCTCCGCAGCAACGCCCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCTCAGAACCTGACCAAGCAGGACATCAGCAGAACAGAT
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCACCAGCCTTCAGCGGCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCATCCCCACCGAGGCGCTGTCCCACCTGCACGCC
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTCAAGAGGC
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCACTTGGACACCATGACACCCAAC
TGCCCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCGTCCGCCACCTAGTCTATCTCCGCTTCTCAACCTCTCCTACAACCCCCATCA
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGC
GGGAGCTGCCGTGGAGGCCCTATGCCTTCCGGCCTCAACTACCTGCGCGTGTCAA
TGTCTCTGGCAACCAGCTGACCAACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCAGCTGTCGGCTCTGTGGTGTCCGG
CGCCGCTGGCGCTCAACTCAACCGCAGCAGCCCACGTGCGCCACGCCAGGTTGTCCA
GGGAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCAACTACTTACCTGCCGCC
CCCGCATCCGGACCGCAAGGCCAGCAGGTGTTGGACGAGGCCACACGGTCAGTT
GTGTGCCGGCGATGGCGACCCGCCCGCCATCCTCTGGCTCTCACCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCCAAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCCGGCAACGAC
TCCATGCCGCCACCTGCATGTGCAGCTACTGCCGACTGGCCCATCAGCCCAACAA
GACCTTCGCTTTCATCTCAACCAGCCGGGAGGGAGAGGCCAACAGCACCGGCCACTG
TGCCCTTCCCCCTCGACATCAAGACCCCATCATGCCACCACATGGCTTCACTCTTT
CTGGCGTGTCTCTTCTGCCTGGTGTGCTGTTCTCTGGAGGCCGGCAAGGGCAACAC
AAAGCACAACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAGGCATCAGCTCCGCC
ACGCCGCCGCCAGTTCAACATGAAGATGATATGAGGCCGGGGGGGGCAGGGACCCCC
GGCGGCCGGGAGGGGAAGGGCCTGGTCGCCACCTGCTCACTCTCCAGTCCCTTCCACCTC
CTCCCTACCCCTCTACACACGTTCTTCTCCCTCCGCCCTCCGCTCCCTGCTGCC
CCAGCCCTCACCACTGCCCTCTACAGGACCTCAGAAGGCCAGACCTGGGGACCCCA
CCTACACAGGGGATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTCA
ATAATTCAATAAAAAGTTACGAACCTTCTGTAACTTGGTTCAATAATTATGGATTT
TATGAAAATTGAAATAATAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTL
GLRSNRKLIPLGVFTGLSNLTQDISENKIVLLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCYLGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMHL
LRLQEIQQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSVGNNLETLLIDSNPLA
CDCRLLWVFRWRNLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARI RDRKAQGV
FVDEGHTVQFVCRADGDPPIALWLSPRKHLVSAKSNGRDTVFDGTLEVRYAQVQDNGTYL
CIAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCACAGCGTCCGACCTCGCCCCGGCTCCGAAGCGGCTGGGGGCCCTTCGGTCAAC
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGGCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATGGGGCCCAACCTCTCCCAGGACAGCCAGCCCTGG
TGTTCGCCTGCTGCTGGCGCCGGGGCCAACCTCTCCCAGGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTCAAGTGCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGCTAACCTGCTCAGCAGACTCTACTTGGGAGAAGA
GAGCCCTCGAGATAATCGAATTCAAGCTGGTACCTCTACGCCAACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTCACTATGCCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCACTGGTT
ATAAAATCTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTCTGGGAGCAAG
CCTGCAGCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCGCAT
ACAGGAAGATCCCAATGGTAAAACCTTCAGTCAGCAGCTCGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGGAGCATCGTGTGCTGTGAACCCTGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAACAGCTGTTGCTACACTGTGAGGGTCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTCCTCAACAAGAGTGAAGTGGCACCTACGGCTGCACAGCCACCAAG
CAACATGGGAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT
CCTCCTCCAGCACCTACCACGCCATCATCGTGGGATCGTGGCTTCATTGTCTCCTGCTG
CTCATCATGCTCATCTTCCCTGGCCACTACTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAGGCTCCGACGATGCTCCAGACGGGACACGCCATCATCAATGCAGAAGGGG
GGCAGTCAGGAGGGACGACAAGAAGGAATATTTCATTAGAGGCGCCTGCCACTCCTGC
GCCCCAGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCGCTTGGCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTGACTCGGTTGGAATGGGAGGGAGGAGGGCGGGGGAGGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA
AACAAAAAACA

FIGURE 32

MGAPAASLLLLLFFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRQLVTSTPHELYSISISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKG
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTCTCCTTCTGG
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGTTAAAAATGCTGCTTGGATTCTGTT
GCTGGAGACGTCTTTGCTGGAAACGTTACAGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTTACCAATTATTCATGGCAATTC
CCTCACTCGACTTTCCATAATGAGTCGCTAACCTTATAATGCGGTTAGTTGCACATGG
AAAACAATGGCTTGATGAAATCGTCCGGGGCTTTCTGGGCTGCAGCTGGTAAAAGG
CTGCACATCAACAACAAGATCAAGTCTTTCGAAAGCAGACTTTCTGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCTT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGCCGAGTGGTCTGCGAAGCCCCACCAAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGCTTTGAAAACCGAGTGGATTCTAGTCTCCGGCCCGCCCTG
CCCAAGAACAGAGACCTTGCTCCCTGGACCCCTGCCACTCCTTCAAGACAAATGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAGATCCCAGGCAACTGGCAGAT
AAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAAC
GTTTACCCCTGCCCTGGGGCTGCAGCTGCGACCACATCCCAGGGTGGTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCAAGCTCTAACGTGCAGGA
GCTTTCTACGAGATAACAAAGATCCACAGCATCCGAAAATCGACTTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGCAACAAATAACATCGTACTGTAGAGAACACACTTCAAG
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCAGGA
GAAATTGCGGGGCTGCAAAACCTAGAGTACCTGAACGGTAGTACAACGCTATCCAGCTCA
TCCTCCGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAAACACCTG
CTGAGGTCCCTGCCTGTGGACGTGTTGCTGGGTCTCGCTCTAAACTCAGCCTGCACAA
CAATTACTCATGTACCTCCGGTGGCAGGGTGCTGGACCAGTTAACCTCCATATCCAGA
TAGACCTCCACGGAAACCCCTGGAGTGCTCCTGCACAATTGTGCCTTCAAGCAGTGGCA
GAACGCTTGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGTGAACCTT
TAGAAAGGATTTATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTAACCGCACAGTAAAACAGCACTGGGTGGCGAGACCGGACGCACCTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTGGTGTGGTCCCAGGACTGCTGCTGGT
GTTTGTACCTCCGCCTCACCGTGGGGCATGCTCGTGTATCCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACTCCTCCCGTCCGAGATTAAATTCCCTACAGACAGTCTGT
GAECTTCTACTGGACAATGGCCTTACAACGCAGATGGGCCACAGAGTGTATGACTG
TGGCTCTACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGAGGGCAGAGGGAGGG
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCAAATCCCGCG
CCATCAGCCTGGATGGCATAAGTAGATAAAATACTGTGAGCTGCACAAACGAAAGGGCT
GACCCCTACTTAGCTCCCTCTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCTTTGCTGAGAGCCCTTTGACAGAAAGCCAGCACGACCCCTGCTGGAAG
AACTGACAGTGCCCTGCCCTGGCCCCGGGCCTGTGGGTTGGATGCCCGGTTCTATAC
ATATATACATATCCACATCTATATAGAGAGATAGATATCTATTTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACCGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAACCTTGACTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENGLHEIVPG AFLGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLRLIDPGAFQDLNKLEVLIILNDNLISTLPANVFQYVPITHLDLRG
NRLKTLPYEEVLEQIPGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDILNETTEQDLCPLKNRVDSSLPPAPAQEETFAPGPLPTFKTNGQEDHATPGSAPNGGT
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSDHIPGSGLKMNCCNNRNVSSLADLKP
KLSNVQELFLRDNIHSIRKSHFDYKNLILLLDGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNQIQLILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
SKLSLHNMYFMYLPPVAGVLDQLTSIIQIDLHGNPWECSCTIVPKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDIECPOLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLLLVFVTSFTAFTVVGMLVFILERNKRKSRDANSASEINSLQTVCDSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC
TGCACCGGGCTGGCAGCGCTCCGCACACATTCTGTGCGGGCTAAGGGAAACTGTTGGC
CGCTGGGCCCGGGGGGATTCTTGGCAGTTGGGGGCTCGTCGGGAGCGAGGGCGGAGGGG
AAGGGAGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGAAC
AGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTGTGCGTGCCTGGGGCCTCAG
AGAATGAGGCCGGCTCGCCCTGTGCGCTCTGGCAGGCCTCTGGCCCGGGCCGGCGG
CGGCGAACACCCCCACTGCGGACCGTGCTGGCTGCGCTCGGGCCTCGGGGCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGGCGAGGAGGCCTGCATCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCAGCTGCGCGCTGTGCTCGCGCTCTGCGGGCAGGCCAGG
GCCCGGAGGGGCTCAAAGACCTGCTGTTCTGGGTCGACTGGAGCGCAGGCCTTCCCAGT
GCACCCCTGGAGAACGAGCCTTGCAGGGTTCTCTGGCTGTCTCCGACCCGGCGGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGGGAGATGCGC
GGTACTCCAGGCCACCGTGGGTGAGGCCGAGGCTGGAAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTCAAGTACCAAGTTGAGGTCTGTGCGCCTGCACCCGGGG
GCCGCCTCTAACTTGAGCTATCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGCGCTCGCTGGACAAACTCTCGGGCGATGTGTTGTGCGCCCTGCC
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAAGTGCCTAGACGACTTGGGAGG
CTTTCGCTGCGAATGTGCTACGGGTTGAGCTGGGAAGGACGGCGCTTGTGACCA
GTGGGGAGGACAGCCGACCCCTGGGGGACCGGGGTGCCACCAGGCGCCGCCGGCACT
GCAACCAGCCCCGTGCCGAGAGAACATGGCAATCAGGGTCGACGAGAACGACTGGGAGAGAC
ACCAACTGTCCCTGAACAAGACAATTCAAGTAACATCTATTCTGAGATTCTCGATGGGAT
CACAGAGCACGATGTCACCCCTCAAATGTCCCTCAAGCCGAGTCAGGCCACTATCACC
CCATCAGGGAGCGTGATTCCAAGTTAATTCTACGACTCCTCTGCCACTCCTCAGGCTT
CGACTCCTCCTCTGCCGTGGTCTTCATATTGTGAGCACAGCAGTAGTAGTGTGTTGATCT
TGACCATGACAGTACTGGGCTGTCAAGCTCTGCTTCAAGAAAGCCCTCTCCAGCCA
AGGAAGGAGTCTATGGGCCGCCGGCTGGAGAGTGATCCTGAGGCCGCTGCTTGGCTC
CAGTTCTGCACATTGCACAAACAATGGGTGAAAGTCGGGACTGTGATCTGCCGGACAGAG
CAGAGGGTGCCTTGCTGGCGAGTCCCTTGGCTCTAGTGATGCAT**AGGGAAACAGGGGA**
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACCTAC
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCCTCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA
TGGTGTACTGGGGACCGGGTAGTGTGCTGGGAGAGATATTCTTATGTTATTGGAGAA
TTTGGAGAAGTGAATTGAAACTTTCAAGACATTGAAACAAATAGAACACAATATAATTACA
TTAAAAAATAATTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT
ATTGGTTGAAATCCCAGGGAAAAAATAAAAATAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPAGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILTMVLGLVKLCFHESPSSQPR
KESMGPPGLESDEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGATT CAGCAGTGGCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCAT AATCGCCTTAAAAGTGCCTCCGCCCTGCCGGCGCGTAC
CCCCGGCTACCTGGGCCGCCCCGCGCGGTGCGCGCGTGAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGAGCGCGGTGTGAGCGCGGTGGGTGCGGA
GGGGCGTGTGCGCGCGCCGGTGC A A A C C C G A G C G T C A G C T G C C A T G A
GGGGCGCGAACGCCTGGCGCCACTCGCCTGCTGGCTGCCGCCACCCAGCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCCCTGGAGTGTACCCCTCAAATAGCAAATGTACTTGAAAATCA
CAGTTCCCAGAGAAAAAGTAGTCGTTCAATTCCGATTCA TAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTGTGGATGTGTACAATGCCATGCCAATGCCAGCGCATTGGCG
CTTCTGTGGCACTTCCGGCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGCCATGTTCTCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTAAAAC
CCCCAACTGCCAGACCGGGATTACCCCTGCAGGAGTCACTTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGATAGTCCACCTCGGCCAATTGTGTCTGAGAGAAATGAACCTTATTCA GT
TTTATCAGACTTAAGTTAACTGCAGATGGTTTATTGGTCACTACATATT CAGGCCAAA
AAACTGCCTACAACACTACAGAACAGCCTGTCACCACCATCCCTGTAACCACGGTTAAA
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGA CTTGTATTAGCCGGCACTGTTATCACAACCACACTCGCAGTGGAGTTG
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTGGCATTGAGCAGGGGG
CAAGAACATGAGTGCAGGCTGACTGTCGTGCAAGCAGTGCCTCTCCTCAGAACAGAGGTC
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGCAAATCATGCCAACAGC
TTTATCATGATGTTCAAGACCAAGAACATCAGAAGCTCCTGGATGCC TAAAATAAGCAATG
TTAACAGTGAACTGTCCATTAAAGCTGTATTGCCATTGCCCTTGAAAGATCTATGTC
TCTCAGTAGAAAAAAATAC TTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAAGTTCTT
TGCCTGCTGTCAAGCGTTGACAGCTGGAAAGCGTTATTTATACATCTGTAAAAGGAT
AGCTAAAAGTGTCAAGCGTTGACAGCTGGAAAGCGTTATTTATACATCTGTAAAAGGAT
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAAGATTTAGAAGTGC AATATTATAGT
GTTATTGTTCACCTCAAGCCTTGCCTGAGGTGTACAATCTGTCTTGCCTTCTA
AATCAATGCTTAATAAAATTTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPD RDYPAGVT CVWHIV
APKNQLIELKFEKFDVERDNYCRYDYAVFNGGEVNDARRIGKYCGDSPAPIV SERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKC RRTGTLEG N
YCSSDFVLAGTVITTITRD GSLHATVSIINIYKEGNLAIQQAGKNMSARLT VVCKQCPLLRR
GLNYIIMGQVGEDGRGKIMPNSFIMMF KTKNQKL DALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCCGGGCTGGGCAGTCGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTACACCTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAACCATCCGGACAACCTTGAG
GTGGAAACACTGCCTGGGAGGAAGAGAACATTGTCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGAACAGAGAGGCCCTGCGGTGGCTACGGCAGTGTGAAGGGAGAAGG
GACACGAGGGGGCAGCGGCACTGTGACTGCCAAGCGGCTACGGGGTGAGGCCTGTGGCC
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCATCTGGTATGTTGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGGTCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAAG
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCAGCAGATGTTCTTGGCATCATCATGTGCACTGGCCA
CGCTGGCTGCTAAGGGCAGTTGGTGTACCGCCATCTCATTGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTCAAGAGCGAGTGACCGTGTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCTCCCACCCACGCTGCCCGAGAGCTTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTTGGTTATTTGAGAGTGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAGGAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTCACCTGGCGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCTGCCAGTTCTGT
TCTGTGTTCACACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAGA
AAGGTCTTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCCGGTERPCGGYGCCEGEGETRGGSGHCDCQAG
YGGECACGQCLGYFEAERNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCVGENKCENCTEGGYRCICAEGYKQMEGICVKEQI PESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAGDLVFTAIFIGAVAAMTYWLSERSDRVLEGFIFKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-363

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
GCACCATGCAGCCCCGTGGCTCTGCTGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGCAGCCTGCTGCCAGCTGAGCTCAAAGAGGT
GCCCACCTGGACAGGGCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTCAGGCCGTGCTGCCCTTCCAGG
AGCCGGTCCCCAAGGCCGCGTGCACAGGCACGGCGGCTGTCCCCGCCAGCGCCGGGCC
CGGGTGACCGTCGAGTGGCTGCGCGTCCCGACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGCCCGCAGCCGCTGCTGCTACAGGTGTCGGTCAGAGG
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGGC
GCCAGCCGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGCCGAGAACTGGTGCTGGAGCCCCCGGGCTT
CCTGGCTTATGAGTGTGGCACCTGCCGGCAGCCCCCGGAGGCCCTGGCCTTAAGTGGC
CGTTCTGGGCCTCGACAGTGCATGCCCTCGGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCTGCCAACAGCCATAGGCGCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGGTGCAGGGTACCAAGGAGAGCTG
GCGATGACTGAAGTGCCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTTGCTCTCAGGAATGAGAACATCTTGGCCACTGGA
GAGCCCTGCTCAGTTCTATTCTTATTACTGCACTATATTCTAACGACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCATTGTTACTTGTCCGTAC
TGGATCTGGCTAAAGTCCTCCACCACCACTCTGGACCTAACAGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTTGTAACATGAATAAACACACATTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEHQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCAGGAGTCCTCGCGGCTGTTGTCAGTGGCCTGATCGCGATGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGCTCTCATATTGGCGATCCTGTTGCTCCCTGG
CATTGGGCAGTGTACAGTGCACCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTCTTCTCCCCGTGGAGTGGAAAGTTGACCA
AGGAGACACCACCAAGACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG
TGACCTTCTGCCAACTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTCTGAATAACACCTGGTCAAAGAT
GGGATACTGATGCCTACGAATCCAAAAGCACCCGTGCCCTCAGCAACTCTCCTATGTCCT
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCCTGTAGCCTCTGATAACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTCAAATGCTGTGCGCATGGAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCCCTGATTCTCCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCTGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTCACCGCCTATCATCTGCATTGCTTACT
CAGGTGCTACCGGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCCTATTGCTTC
TACACCCCACAGGGCCCCCTACTTCTGGATGTGTTTAATAATGTCAGCTATGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCTGGAACCTGTTAAA
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAAGTAGACAGAAAAATGGCGGGGTGCGAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTTGAGCTGGTCTGGCTCTTCCATTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTGCTTCCATTGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCCCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAAATGGAGCTTTGTTGGAGAGCATAGTAAATTTCAGAGAACCTGAAGCCAAAAG
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAAGACTGGAGGCTGGCGCAGTGGCTACGCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGAGTTGGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEGFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGC**A**TGAGCGGCGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCGCTTCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG
GCTCGTGCCCACCCACCAAGTTCCAGTGCCGACCAAGTGGCTTATGCGTGCCCCCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCAACCGCCCCCTGGCCTCCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCCCTGTGCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGTTATTGCAGCTGCTGCCGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCCTCCTCTTTGTCCTGGCTCCGAGCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAACAGAC
CTCGCTGCC**T**GAGGACAAGCAGTGGCACCCGAGCTCAGCAGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGTACCCGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACAGAC
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCDRDLDSDGSDEEECRIEPCQKGQC PPPGLPCPCTGVSDCSGGTDKKL
RNCSRRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCACCGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGAGCAGAGGTGCACAGATGCC
GTTAGACTGGCGGGGGAGGAGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCACACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTTAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTCAAGTGTGCTGACCCGGCATTCCCAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTCTTGAAGGCTCTGTAGCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCTAGGCTGGATCCAAGTGA
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA
ACAAGACATATAGACATGGAGAGAACGTAATCATCACTTGTATGAAGGATTCAAGATCCGG
TACCCGACCTACACAATATGGTTCAATTATGCGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT
GATGGGTCTGCGTATCTGAGTGCTTACAAAACCTTATCTGGTGTCCAGCCCACCCGGTG
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCAAATGGTGTGAGTCACGGAGATTCGTCT
GCCACCCGCGGCCCTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTACTGCGATCCT
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGGTGTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCTCCCCGGAG
TTCCAGCAGTGACCTGACTTGTGGTAGACGGCGTGTGCTGCTGCTCGTCATGCTCCGTCTATG
ACGAAGCTGTGAGTGGCGCTTGAGTGCCTAGGCCCGGGTACATGCCCTCTGTGGGCCAG
GGCTGCCCTTACCCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTGAGCTGCTCCAAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCTGCTGGACAACCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATGCCACTGGGT
GTTGTTCTAAGAAACTGATTGATTAAAAATTCCAAAGTGTGCTGAAGTGTCTTTCAA
ATACATGTTGATCTGTGGAGTTGATTCTTCTCTGGTTAGACAAATGTAACAA
AGCTCTGATCCTAAAATTGCTATGCTGATAGAGTGGTGGAGGGCTGGAAGCTGATCAAGTC
CTGTTCTTCTGACACAGACTGATTAAAATTAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGVFFEGSVARFHQCQDGFKLGATKRLCLKHNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCAGTCGGTCCGTGGCTAGAGA
TGCTGCTGCCCGGGTTGCAGTTGTCGCACGCCTCTGCCCGCAGCCGCTCCACCGCCGT
AGCGCCCGAGTGTGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGAAACCGCGCTACAGG
CCGTGCTGCCGTGCTGGTGGGGCTGCCGGCGACGGGTCGCCTGCTGAGTGCC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTTGTAA
TAAAGTCATTACTTCATGATACTTCTGAAGACTGAACCTTGAGGAAGCAAAGAACGCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTTCATGAAAACCTCTGCCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT
CACAAATTAGGAACGGTATGGATGAGCCGTCCTGCCAGCGAGGTCTGCCGTGGTCATG
TACCATCAGCCATGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACAAATTCTTGCACAAATTCTGATGAGAAACCAGCAGTTCC
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG
GAAGAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAACGCTGCCCTGAATCTGCCCTACAT
CCTAATCCCCAGCATTCCCCTCTCCTCCTCTGTGGTCAACCACAGTTGTATGTTGGTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAACACACCATC
TGGCCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTCATTCCGAGTGTGTT
CGGGAGAAGCCACTCCGATGACATGTCTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACCAATGGGAGGAGTAAGGAGTCTGGATGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAACTGAAACTGACAACAAATGGAAAGAAATGATAAGCAAATC
CTCTTATTTCTATAAGGAAATACACAGAACAGTCTATGAACAAAGCTTAGATCAGGTCTGT
GGATGAGCATGTGGTCCCCACGACCTCTGTGGACCCCCACGTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAACGGTACCTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCACTTGGTTGGTTGTATCTAACCTTAAGGGACAGAGCTTACCTG
GCAGTGATAAAAGATGGGCTGTGGAGCTGGAAAACCACCTCTGTTCTGCTATACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAACATCTTCAAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATGGCAATTCTCATATCTGTTCTCAAAGAACAAATCAAATAAAGA
GCAGGAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGQTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIEKFIEPLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKY
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKTFKESREAALNAYILIPSIPLLLLLLV
VTTVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSEGFTLVSVESGFVTNDIYEFSPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCC CGGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
GTT CAGCATGCGTTGTGGACCCCAGTGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTGCACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGT CGT GTT CGACACGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGC
GCAGCAAATGTTGCCTGGGAGAGAGACTGAGGAAGAACTATGTGGAAAGACATTCCCTTC
TTTCACCAACCTTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATT CAGAAGTCTTGTATCCA ACTACCAAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGT GATAAAAGTGGACTTCTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGACTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATT CCTCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG
TGACCTTCATACCGCTTTAATGACCCCTGGGATTTTGACCACAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACCTTACCA GCACTGGAAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACCA CGGG AAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSFYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRTASLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHLNPSCPMLKRFARMIEQRRAVDTSLYILPKEDRESLQMAVGPFLHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTAACATACTTGCAGCTAAAACAAATATTGCTGCTGGGGACCTCCTCTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTGCAACCAGACCTGGATTCCTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGCACCGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTTTCTCCCCA
GTCCCAGAGGGTGTCAAGGCTGGCTGACGGCCCTGGCATTGCAAGGGACCGTGGAGTGAA
GCACCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGAAAGGTGG
TGTGCCGGCAGCTGGATGTGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCTTCA
GGATTGCCCTCTGGCCTTGGGGAAAGAACACCTGCAACCAGATGAAGACACGTGGTCG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGCTCTGCTGTGATGACAACACTGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGCTGTGGAAGTCCCTCTCCCTCAGAGACCGGA
AATGCTATGCCCTGGGTTGCCGCATCTGGCTGGATAATGTTGTTGCTCAGGGAGGAG
CAGTCCCTGGAGCAGTGCACAGATTTGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGAGCATTACTGTCTACATGACTGCATGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGACTTAACTTGGTGCCTGATTCTCAGGCCTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGAACACTACATCA
CCACCTTCCTATGTCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTGTAT
CAAACACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA
CACCAATTGTCCTGTTCTGTGAAGAACTCTGACAAAATACAGATTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGAATTGGTTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTATTACAATAATAAGATAGCAC
TATGTGTTCAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGLHRCEGRVEEQKGQWGTVCDDGWDIKDVAVL
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGRHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPDFDLRLVG
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIDL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTGACCTCGAC
CCACCGCGTCCCGGGACCGTGGCGGACCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCACAGCCATCCTGCCCTGCTGTTGGCTGCCCTGG
CGTCTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAAATGGTGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCTGAGATCCTGCAGTGCTTGCTATGTC
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACACCAGTGG
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGGAGGAAGGCCACATTGTGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCCCTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTG
CTGTCTCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATCACCGGGATGGATCTAGGTATGGAGTTATGGAC
ACCACACAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGTGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTGGCTGTTATCTCGAA
CTCTGGCTCCTGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTGCTCTACAAGTGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA
AGCTTCTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAGGGCGGCCGCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCATGGCCCAACTGTTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVTGATSGLGKECAKVFYAAGA
KLVLICRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL
VNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKS KNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCACCGCGTCCGCTGGTGTAGATCGAGCAACCTCTAAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTCTTGACATCCTC
CTGCTTCTCCCCTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCTAA
GAGGAGAAAATCAGTCACCGGGAAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA
GAUTGACTGCCTATGAATTGCTAAACTAAAGCAAGCTGGTCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAATGCAAGGGACTGGTGCCAAGGTTCATACCTTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGACACATTCTGGACTACAAA
GGCATTCTTCTGCAATGACGAAGAATAACCATTGGCCATATTGTCAGTGTGGCTTCGGCAG
CTGGACATGTCTCGGCCCCCTTACTGGCTACTGTTCAAGCAAGTTGCTGTTGG
TTTCATAAAACTTGACAGATGAACACTGGCTGCCTACAAATACTGGAGTCAAAACAACATG
TCTGTGTCCTAATTGTAACACTGGCTTCATCAAAATCCAAGTACAAGTTGGGACCCA
CTCTGGAACCTGAGGAAGTGGAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG
ATTTTATTCCATCTCTATAGCTTTTAAACAACATTGGAAAGGATCCTCCTGAGCGTT
CCTGGCAGTTTAAAACGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATAAGCACCTAGTTCTGAAAATGATTACCAAGTTAGGTTGATGTCATCTA
ATAGGCCAGAATTAAATGTTGAACCTCTGTTTTCTAATTATCCCCATTCTCAATA
TCATTTTGAGGCTTGGCAGTCTCATTACTACCACCTGTTCTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTAGAGGTGACTTAAGGAAAATGAAGAAAAGAA
CCAAAATGACTTATTAAAATAATTCCAAGATTATTGTGGCTCACCTGAAGGCTTGCAA
AATTGTACCATAACCCTTATTAAACATATATTATTATTGATTGACTTAAATTGTT
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTTCAGCTCTCAATGGTAGGTT
TGAAGGACTATATCTAGTGGTATTTCACAATGAATATCATGAACCTCTCAATGGTAGGTT
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACTCACATTCAATGCCAACATTCT
GCACAGGGAAAGCTAGAGGTGGATACACGTGTGCAAGTATAAAAGCATCACTGGATTAAAG
GAGAATTGAGAGAAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA
AA

FIGURE 58

MKFLLDILLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSI LVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCACCGCGTCCGGACCGTGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGCGCTC
AGGGAGGAGCACCGACTCGGCCGCACCCCTGAGAGAATGGTGGTGCCATGTGGAAAGGTGATTG
TTTCGCTGGTCCTGTTGATGCCCTGGCCCTGTGATGGGCTGTTCGCTCCCTATACAGAAGT
GTTTCATGCCACCTAACGGAGACTCAGGACAGCCATTATTCTCACCCCTTACATTGAAGC
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTGGCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCCTCACCGTAATAAGACTTACAACAGCAACCTCTCTGGTTC
TTCCCAGCTCAGATAACGCCAGAACGATGCCAGTAGTTCTCTGGCTACAGGGTGGGCCGG
AGGTTCATCCATGTTGGACTCTTGGAACATGGCCCTATGTTGTACAAGTAACATGA
CCTTGCCTGACAGAGACTTCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTACTGATGATAACCCACGGATATGCAGTCATGAGGACGATGT
AGCACGGGATTATACAGTCACTAATTCAAGTTCCAGATAATTCTGAATAATAAAAATA
ATGACTTTATGTCACTGGGAGTCTTATGCAGGGAAATATGTCAGCCATTGCACACCTC
ATCCATTCCCTCAACCTGTGAGAGAGGGTAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGCAGAAATTCTGTACCAAATTGGCT
TGTTGGATGAGAACAAAAAGTACTTCAGAAGCAGTGCCTGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAAACTACTAGATGGCAGCTAAC
AAGTGATCCTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCGGT
GCACGGAACCTGAGGATCAGCTTACTATGTAATTGTCAGCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGAACTATAGTTGAAAGTACTTGCAGA
AGATACAGTACAGTCAGTTAACCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAACGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCTTGATGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAACGGAGAAAAAGTTGGAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATC
GAGGTGGAGGACATATTTACCTATGACCAGCCTCTGAGAGCTTGACATGATTAATCGA
TTCAATTATGAAAAGGATGGATCCCTATGTTGATAAAACTACCTCCAAAAGAGAACAT
CAGAGGTTTCATTGCTGAAAAGAAAATCGTAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTCATATCTGCAAGATTTTCTCATCAATAAAAATTATCCTGAAACAAGTGAGC
TTTGTTTTGGGGGAGATGTTACTACAAATTAAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAATGA
AATTAAAGGGTCTGAAATAGGAAGTTTAATTCTCTAAGAGTAAGTGAAGGAGTCAGTTG
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT
GTTGGAAATATTATGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA
TAGTTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTGAAATA
AAAATATTATATAAAAGTAAAAAAAAAA

FIGURE 60

MVGAMWKIVSLVLLMPGCDGLFRSLYRSVSMPKGDSGQPLFLTPYIEAGKIQKGRELSL
VGPPFPGLNMKSYAGFLTVDNKTYSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLRDRDFPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSNLPREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFQAFEILDKLLDGLTSDPSYFQNVTG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEKVWKIFKSDSEVAGYIRO
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTCCGGCTCCGAATGGCACATGTGGGATCCCAGTCTTGGCTACAACAT
TTTCCCTTCTAACAAAGTCTAACAGCTGTTCAACAGCTAGTGATCAGGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTACCGCTCCTG
CCTCTCTGTTGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTGTGTCATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGGAGGGCCTGCCAACAGCTTCAAAAAACAGGAGCGACTTCACTGGCTGGGAT
AAGACGTGCCGTAGGATAGGAAAGACTGGTTAGTCATAATCAAATTGACTGGCTGGG
TGAACCTAACAGCCTTTAACCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTGTAAAATAAATTAAAATTTAAAAAAGCAAGTATTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAACAGGGAGAAAGTATGTTAAAATA
GAAAAACAAAATGCAGAAGGAGGAGACTCACAGAGCTAACACCAGGATGGGACCTGGGTC
AGGCCAGCCTTTGCTCCTCCGGAAATTATTTGGTCTGACCACTCTGCCTGTGTTT
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
ACAGCCGCTCTGGTCTCTCAGTGGCTGGGTGCTGCTGGCCCCCAGCAGCCGGC
ATGCTCAGTCAGCACCTCCACTCTGAGAACATCGTGAUTGGACCTCAACCACCTGACCGT
CCACCAAGGGACGGGGCGTCTATGGGGGCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTATAAGACAGGGCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCCCATCGTGCAGCCCTGAGCGAAGTGCACCCCTACCAACAATGTCAACAAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGAGCCTCTACCAGGGGTCTGCA
AGCTGCTGCCGTGGATGACCTCTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCAGTGTCAACAAGACGGGACCATGTACGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCTGTCCA
GCCGGAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCCACCTTGACAT
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCCGAGA
CCCCTGAGGGTGTGGCATCAACTCCGCTGGAGACCTCTACACCTCACGCATCGTCCGG
CTCTGCAAGGATGACCCAAAGTCCACTCATACGTGCTCCCTGCCCTCGGCTGCACCCGGC
CGGGTGGAAATACCGCCCTCTGCAGGTGCTTACCTGCCAACGCTGGGACTCACTGGCCC
AGGCCTCAATATCACCAGCCAGGACCGATGACTCTGCCCTGTGCTCCCTACCGGCAACTGGAGCTCAACTGGC
CACTGAGGAGCCTGCAGTCTGCTACCAAGGGCAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGAAGGACGTCCAGTGCACGAAGGCGCTGTCCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCCCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTG
TGGGGACTAAGAGTGGCAAGGAGCTGAAAAAGGTAAGAGTCTATGAGTTAGATGCTCCAATGCC
ATTCACCTCCTCAGCAAAGAGTCCCTTGGAGGCTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTTATTTCTTGGGAACAAAGGTGAAATGGGAGGTAAGAAGGGTTAATTTGTG
ACTTAGCTTCTAGCTACTTCCAGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA
TTTCAATATTCCCAAACCTTAAGAAAAACTTTAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSRSVVLSSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKL TGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKL IIIDYS ENRLLACGSL
YQGVCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTM YGVI VRSEG EDGKLF IGTAVDGKQDY
FPTLSSRKLP RDPESSAMLDYELHSDFVSSLIKI PSDLALVSHFDIFYIYGFASGGFVYFL
TVQ PETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSL A QAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEGN
LELNWL LGKD VQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTS VASYVYNG
YSVVFVGTKSGKLKKVRVYEFRCSNAIHLLSKESLLEG SYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGGGCTGAGTGC GG ACTGGAGTGGGAACCGGGTCCCCGCGCTTAGAGAACACCGCATGACCA
CGTGGAGCCTCCGGCGAGGCCGGCCGCACCGCTGGGACTCCTGCTGCTGGCTCTGGGCTTCCTGGTGCCTCC
GCAGGCTGGACTGGAGCACCCCTGGTCCCTCTGGGCTCCGCATCGACAGCTGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTCTGGATCTCGGGGCTCCATCCACTATTCCGTGTGCCAAGGGAGTACT
GGAGGGACCGCTGCTGAAGATGAAGGCCTGTTGAACACCCCTCACCACTATGTTCCGTGAAACCTGCATG
AGCCAGAAAGAGGCAAATTGACTTCTCTGGGAACCTGGACCTGGAGGCCCTCGTCTGATGGCCAGAGATCG
GGCTGTGGTGATTCTGCTCCAGGCCCTACATCTGCAGTGAGATGGACCTGGGGCTTGCCAGCTGGCTAC
TCCAAGACCCCTGGCATGAGGCTGAGGAACAATTACAAGGGCTCACCGAAGCAGTGGACCTTATTGACCAC
TGATGTCAGGGTGGTGCACCTCCAGTACAAGCGTGGGGACCTATCATTGCGTGCAGTGAGAATGAATATG
GTTCTATAATAAGACCCCGACATGCCCCTACGTCAAGAAGGCACTGGAGGCCGTTGGAACCTGGAACCTGC
TCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCAGGGACTCTGGCCACCATCAACTTGCAGT
CAACACAGGACTGCAGCTACTGACCACTTCTCAACGTCAGGGACTCAGGCCAAGATGGTGTGAGGAGT
ACTGGACGGGGTGGTTGACTCGTGGGAGGCCCTCACAAATATCTGGATTCTCTGAGGTTTGAAAACCGTGT
CTGCCATTGTGGACGCCGCTCTCCATCAACCTCTACATGTTCCACGGAGGCCAACCTTGGCTTCAATGAAATG
GAGCCATGCACCTCCATGACTACAAGTCAGATGTCACCACTGACTATGATGCTGTGACAGAAGCCGGCG
ATTACACGGCCAAGTACATGAAGCTCGAGACTTCTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG
ACCTTCTCCCAAGATGCGTATGAGCCCTAACGCCAGTCTGTACCTGCTCTGTGGACGCCCTCAAGTACC
TGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCTC
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGATCGGGGCGAGG
TGTGTTGAACACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGATGCTGTCCCCCTGATCCAGGGTT
ACACCGTGTGAGGATCTGGTGAGAATCGTGGCGAGTCACATGGGGAGAATATTGATGACCAAGCGCAAAG
GCTTAATTGAAATCTCATGATGATTACCCCTGAAAAACTTCAGAACATAGCCTGGATATGAAGAAGA
GCTTCTTTCAGAGGTTGCCCTGGACAAATGGNTTCCCTCCAGAAACACCCACATTACCTGCTTTCTTCTGG
GTAGCTTGTCCATCAGCTCACGCCCTGTGACACCTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTTGATTCA
TCAATGCCAGAACCTTGACGTTACTGGAACATTGGACCCAGAACAGCCTTACCTCCAGGTCCCTGGTGA
GCAGCGGAATCAACCAGTCATGTTTGAGGAGACGATGGGGCCCTGCATTACAGTTCACGGAAACCCCCC
ACCTGGCAGGAACCACTAACAGTTGAGCGTGGCACCCCTCTGCTGGTGCCTGGGAGACTGCCGCTC
CTCTTGACACTGAAGCCTGGCTGCTGCCACCCCTCACTGCAAAAGCATCTCTTAAGTAGCAACCTCAGGG
ACTGGGGCTACAGTCTGCCCTGTCTCAGCTCAAAACCTAAGCCTGCAGGGAAAGGTGGGATGGCTCTGGGCC
TGGCTTGTGATGATGGCTTCTACAGCCCTGCTTGTGCGAGGCTGTCGGGCTGTCTAGGGTGGGAGC
AGCTAATCAGATGCCAACGCTTGGCCCTCAGAAAAGTGTGAAACAGTGCCTTGTGACCCGAGCTCACAGCCC
TGCAGCATCTGCTGGACTCAGCGTGCTTTGCTGGTCTGGGAGGCTGGCCACATCCCTCATGGCCCCCAT
TTTATCCCCGAAATCCTGGGTGTGTCACCAGTGAGGGGTGGGAAAGGGGTGTCTCACCTGAGCTGACTTTGTT
CTTCTCTCACAAACCTCTGAGCCTTCTTGGGATTCTGGAAAGGAACCTGGCGTGGAGAAAATGTGACTTCCCC
TCCCTCCCACTCGCTGCTCCACAGGGTGACAGGCTGGCTGGAGAAACAGAAATCCTCACCTGCGTCTTCC
CAAGTTAGCAGGTGTCTGGTGTGTCAGTGAGGAGGACATGTGAGTCTGGCAGAACGCCATGGCCCATGTCTGCA
CATCCAGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCCCATGTCTGCAACATCC
AGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCCCATGTCTGCAACATCCAGGG
GGAGGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCCATGTCTGCAACATCCAGGGAGGAGG
ACAGAACGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCACGCCAACAGCAGGGGAGAGCAGGCCACTGGCTTGGG
GAAGTGTGTCCAAGTCCGATTTGAGCCTTGTCTGGGGCCAGCCAAACACCTGGCTTGGGCTACTGTCTGA
GTTGCAGTAAAGCTATAACCTGAATCACAA

FIGURE 64

MTTWSLRRR PARTL GLLL VVLGFLV LRRLDW STLVPL RL RHL QAKGWN FM LEDST FW
I FGGS I HYFR VP REYWR DR LLK MKAC GLNT LTT YVP WNL HEP ERG KF DF SG NLD LEAF VL MA
AEI GLW VILR PG PYIC SEMD LGGL PSW LLQD PGM RL RTTY KG FTEA VD LY FDH LMS RVV PLQ
Y KRGG PI IA VQ VEN EY GS YN KDP AY MPY VK KA ED RG IVE LLT SDN KDG LSK GIV QGV LAT
IN LQ STHE LQL TTFL FN VQ GT QPK MVME YWT GWFD SW GGPH NI LD SSE VL KT VS AIV DAGS
S IN LYMF HG GT NF GFM NGAM HFHD YK SDV TSY DYDA VL TEA GD YTA KYM KLR DFF GS IS GIP
L PPPP DLL PK MP YEPL TP VL YLSL WD ALK YL GE PI KSE KPI N M ENLP VNG NGQ SF GYI LY
TSIT SSG ILS GHV HDRG QVF VNT VSI GFL DYK TT KIA VPL I QGY T VL R I L VEN RGRV NY GEN
ID DQR KGL I GNL YL ND SP LKN FRI YSL DMK KS FF QRF GLD KWX SL PET PT LPA FFL G SLS IS
S TPCDT FLKLEG WEKG VVF ING QNL GRY WNI GPQ KTL YLPG PWL SSG IN QVIV FEET MAG PA
LQFTET PHL GRN QYIK

TOP TO BOTTOM
PREDICTED DOMAIN

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGTGGACGGTCCAGGACC
CTGGTGAGGGTTCTACTTGGCCTTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGCTCGGCCGAGGCCCCCAGGACCTCCATCTCCAATGTTGGAGGAATC
CGACACGTACGGTCTGTCGGCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
AAGAAGCTGTCCTGCCTTCGTTCCCTGCTGCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTGTTCGTAGTGGATAGGGTCATGACCGGTTCTCCTAGACGGGGCC
CGTCCGCTATGTGTCGGCAGCCTGCACTACTTCGGTACCGCGGGTCTTGGGCCGAC
CGGCTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTATGTGCCCTGGAACTA
CCACGAGCCACAGCCTGGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCCTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCCATCCTGGTGTGCTCGAAAACCTGAAATTCTAAGAACCTC
AGATCCAGACCTCCTGCCGAGTGGACTCCTGGTTCAAGGTCTGCTGCCCAAGATATATC
CATGGCTTATACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGCTCTCCGTGACTGCTAGG
AGAAAAGATCTGCTCTCACACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GAECTATACCACTGTAGATTGGCCAGCTGACAACATGACCAAAATCTTACCCCTGCTT
CGGAAGTATGAACCCCATGGGCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA
CTGGGCCAGAATCACTCCACACGGTCTGTGTCAAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG
AATGGTGCCATAAGAAGGGACGCTCCTCCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCACACCTAACGCTTTTGCTCTGAGATGTCATCAGCAAGT
TCCAGGAAGTTCCCTGGACCTTACCTCCCCGAGCCCCAAGATGATGCTGGACCTGTG
ACTCTGCACCTGGTTGGCATTACTGGCTTCTAGACTTGCTTGCCTGGCCCGTGGCCCAT
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGTACC
GAACCTATATGACCCATACCATTTTGAGCCAACACCATTCTGGTGCCAAATAATGGAGTC
CATGACCGTGCCTATGTGATGGATGGATGGGTGTTCCAGGGTGTGGAGCGAAATATGAG
AGACAAACTATTTTGACGGGAAACTGGGTCCAAACTGGATATCTGGTGGAGAACATGG
GGAGGCTCAGCTTGGTCTAACAGCAGTGAACAGGCTGTGAAGCCACCAATTCTG
GGGCAAACAATCCTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTGTGAAGTG
GTGGTTCCCTCCAGTTGCCAAATGCCATATCCTCAAGCTCTTCTGGCCCCACATTCT
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGTTAACCTGGCCGTACTGGACAAAGCAGGGCC
ACAACAGACCCCTCACGTGCCAAGATTCTGCTGTTCTAGGGAGCCCTCAACAAAATA
CATTGCTGAAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGCACTGAAAGGTAGGCCGGCATGGTGGCTCATGC
CTGTAATCCCAGCACCTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA
CCAGCCTGGCAACATGGTAAACCCCGTCTCCACTAAAAATACAAAAATTAGCCGGCGTG
ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIIISIQVENE
YGSYRACDFSYMRHLAGLFRAALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPhGPLVNSEYYTGWLWQNHSTRSVSAVTKGLENMLKLGASVNMYMFHGGSNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPGLPPPSPKMM
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRSLFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLVYVPRFLLFPRRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTGAAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGATACTTGAAGGAATATT
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGCACATTCCAGATGTCAAAAACGATT
GCGTTCCCTTCTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAAGAGTTAGTGAAGAAATAACTTAGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGGTGCCGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAACGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTAGCTTCTCGCGATCACTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGTGTATTGCTCAAAA
CCTTCGAGAGTTGACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTAACAAAGTTAGTCATTCAATGACGGCAC
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAACAGGAACGGAT
TTAAAGTCCAATAACATTGCACAATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT
GACTTGTAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTTATTACCCATGTCA
AAAACTTGGAGTCACTTATTCTCTAACACAAGCTCGAACCTTACAGTGGCAGTATT
AGTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAAACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTAAATGCATAAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC
TCACCTCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGCCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTGTTG
TGGAAGATCACCTTTGATAACCCGCCACTCGAACGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAAATGGATTTAAACTAACGATAATATATGCACAGTGTGAGGAAAC
AACTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG
ATACATCTTTAAAATAAAACAGAGAGGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGTTAGGGTTAAAGTCATTCAACATTGCTGCTGCTAAAGTAAATGATTAAATTGACATT
AAAGGAAAGAAAAATTATAACTAAATCTTGAAGGCTTCTTTAAATTGTTGTAACGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTGCCGCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLROHISRNAQDKQELHLFMLSG
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLESLRELRLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCELERIPHAIIFSLSNLQELDLKS
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTISSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNCNDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCCA CGCG TCGGGC TTCT CTGG ACTT GCATT CCATT CCTT CATT GACA AA ACTG ACTTTTT ATTCT
TTTTTCCATCTCTGGGCAGCTGGGATCCTAGGCCCTGGGAAGACATTGTGTTTACACACATAAGGAT
CTGTGTTGGGTTCTCTTCCCTCCCCTGACATTGGCATTGCTTAGTGGTTGTGGGGAGGGAGACCACGTGG
GTCAGTGCTTGCTGCACTTACTGCCTAGGTACATCGAAGTCTTGACCTCCATACAGTGATTATGCCTGTC
ATCGCTGGTGTATCCTGGCGCCTGCTCTGCTGATAGTGTGCTGCTCTGCTTACTTCAAAATACACAAAC
GCGCTAAAAGCTGCAAAGAACCTGAAGCTGCTGCTGTA AAAAATCACAAACCCAGACAAGGTGTGGTGGCCAAG
AACAGCCAGGCCAAACCATGGCACGGAGCTTGTGCTGCCCTGAGTGTGAAGGATATAGAATGTGTGCC
AGTTTGATTCCCTGCCACCTTGCTGTCGACATAATGAGGGCTCTGAGTTAGGAAAGGCTCCCTCTCAA
GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTGTGATGTGAGGCCAGAAGAAAGGCACAG
CTCCCCATCAGTTCATGAAAATAACTCAGTGCTGCTGGGAACCACTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGCAACCCCTCAGGAAGGAGTTGGGGAGAGAGAACCCACTGTGGGAATGCTGATAAAACCAGTCA
CACAGCTGCTCTATTCTCACACAAATCTACCCCTGCGTGGACTGACGTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCCTATAAAGCTGTCGGCTTAAGGCTGCCAGGCCCTGCCAAAATGGAGCTTGT
AGAAGGCTCATGCCATTGACCCCTCTAATTCTCTCTGTTGGCGAGCTGACAATGGGGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGGTGCCTAATGGCAGAGACCCACAAGGCCATGATCCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAGACCAAGAAAACAAAGCATCAGAATTATCTTCTATGTCCAGCTT
GATCCAGATGGAAGCTGTGAAAAGTGAACATTAAAGCTTTGACGGAACCTCCAGCAATGGGCCTGTAGGG
CAAGTCTGCAGTAAAAGACTATGTCCTGTATTGAAATCATCAGTACATTGACGTTCAAATAGTTACT
GAETCAGCAAGAATTCAAAGAACTGTCTTGCTTCTACTACTTCTCTCTAACATCTATTCCAAACTGT
GGCGGTTACCTGGATACCTTGGAGGATCCTTCAACCAGCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT
TGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTAAACTCAAAGAGATTTCCTAGAAATAGAC
AAACAGTGC AATTTGATTTCTTGCATCTATGATGGCCCTCCACCAACTCTGGCTGATTGGACAAGTCTGT
GGCCGTGTGACTCCCACCTCGAATCGTCATCAAACCTCTGACTGTGTTGTCTACAGATTATGCCAATTCT
TACCGGGGATTCTGCTTCTACACCTCAATTATGAGAAAACATCAACACTACATCTTAACTTGTCTTCT
GACAGGATGAGAGTTTATAAGCAAATCCTACCTAGAGGTTAACTCTAATGGAAATAACTTGCACACTAAA
GACCCAACTTGCAGACCAAAATTATCAAATGTTGGAATTCTGCTCCCTTAATGGATGTGGTACAATCAGA
AAGGTAGAAGATCAGTCAATTACTTACACCAATAATCACCTTCTGCTCATCCTCAACTTCTGAAGTGTACCC
CGTCAGAAACAACTCCAGATTATTGTGAAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA
GAAGATGATGTAATACAAAGTCAAATGCACTGGCAAAATAACACAGCATGGCTTTGAAATCCAATTCA
TTTAAAAGACTATACTGAAATCACCATATTATGTTGAAACCAACTCTTGTCAAGTTAGTCTGCAC
ACCTCAGATCCAAATTGGTGGTTCTGATACCTGTAGAGCCTCTCCACCTCTGACTTTGCATCTCCAAACC
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAAACTTGTAAAGGTGTATCCCTTATTGGACACTATGGGAGA
TTCCAGTTAATGCCCTAAATTCTGAGAAGTATGAGCTGTGTTCTGAGTGTAAAGTTGATATGTGAT
AGCAGTGACCACCAGTCTCGCTGCAATCAAGGGTGTGCTCCAGAAGCAAACGGAGACATTCTCATATAATGG
AAAACAGATTCCATCATAGGACCCATTGCTGAAAAGGGATCGAAGTGCAAGTGGCAATTCAAGGATTTGAGCAT
GAAACACATGCGGAAGAAACTCCAAACCAAGCCTTCAACAGTGTGCACTGTGTTCTCATGGTTCTAGCTCG
AATGTGGTACTGTAGCGACAATCACAGTGAGGCATTGAAATCAACGGGAGACTACAAATACCAAGAAGCTG
CAGAACTATTAACTAACAGGTCCAACCTAAGTGAGACATGTTCTCCAGGATGCCAAGGAAATGCTACCTCGT
GGCTACACATATTATGAATAATGAGGAAGGGCTGAAAGTGACACACAGGCCTGCATGTAAAAAAA

FIGURE 70

MELVRRLMPLTLIILSCLAE LTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIIFS YVQLDPGSCESENIVFDGTSSNGPLLGVCSKNDYVPVFESSSSTLT
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLIEDKQCKFDLAIYDGPSNTNSGLIGQVCRVTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIIITFSASSTSEVITRQKQLQIIVKCEMGNST
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFN AFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVSRSKRD ISSYWKTD SII GPIRLKRDRSASGNSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCCAGGAGCTCCCAGGCTCGCGTCTCGCTGCTGTTGCTGCTGC
TGCTGCCGCCGCCGTGCCCTGCCACAGCGCCACGCCGCTCGACCCCACCTGGGAGTCC
CTGGACGCCGCCAGCTGCCCGCGTGGTTGACCAGGCCAAGTCGGCATCTCATCCACTG
GGGAGTGTGTTCCGTGCCAGCTCGGTAGCGAGTGGTCTGGGGTATTGGCAAAAGGAAA
AGATACCGAAGTATGTGGAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT
TTTGGACCACTATTACAGCAAAATTTTAATGCCAACAGTGGGCAGATATTTCAGGC
CTCTGGTGCCAATACATTGTCTTAACCTCCAAACATCATGAAGGCCTTACCTTGTGGGGT
CAGAATATTGTGGAACCTGGAATGCCATAGATGAGGGCCAAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTGGACTGTACTATTCCCTTTGA
ATGGTTTCACTCCGCTCTCCTTGAGGATGAATCCAGTCATTCCATAAGCGGCAATTCCAG
TTTCTAACAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAAACTGGAACAGCACAGGCTCTGGCCTGGTT
ATATAATGAAAGCCCAGTTGGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTACCTGCAGTGATCGTTATAACCCAGGACATCTTGCCA
CATAAATGGGAAAATGCATGACAATAGACAAACTGTCTGGGCTATAGGAGGAAAGCTGG
AATCTCTGACTATCTAACATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTCATGTG
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTTCTGTAGTTTGAG
GAGCGACTGAGGCAAGTGGGTCTGGCTAAAGTCATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTCTAAATGGCCCACATCAGGACAGCTGTTCTGGCCAT
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAAC
GATTCTTGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCAGATGC
CGTGTAAATGGGGCTGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAAACTGGATAAGAAAATTATTGGCAGTTCAAGCCCTTCCCTTTCCACTA
AATTCTTCTAAATTACCCATGTAACTCTCCAGTGCACTTGCCATTAAAGTC
TCTTCACATTGATTGTTCCATGTGTGACTCAGAGGTGAGAATTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTGTGAAGCCATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCATTGCTAGTCAT
TTTTTTGTGCCAACATCATAGAGTGTATTACAAAATCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAATACTGTAAATAATGGTGACCTGTATAGGGCACTTACCCACGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTATAAAAAAAA
GTTTTCTTCTTCATTATAAATTAACATAAGTGTACTGTAACATTACAAACGTTTAATT
TTTAAACCTTTGGCTTTGTAATAACACTAGCTAAACATAAAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHG
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNTQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETY
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNW
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGCCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTGCAGCAGAAGAGCT
TTCCATCCAGGTGTCATGCAGAATTATGGGATCACCCCTGTGAGCAAAAAGGCAGACCAGC
AGCTGAATTCACAGAACGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAAACTTGCAAGCTATGGCTGGGTTGGAGA
TGGATTCTGGTCATCTAGGATTAGCCAAACCCAAAGTGTGGAAAAATGGGTTGGGTG
TCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACTCATCTGAT
ACTTGGACTAACCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATTCAACACTCA
AACTGCAACACAAACAGAACATTATTGTCAAGTACCTACTCGGTGGCATCCCCCTT
ACTCTACAATAACCTGCCCTACTACTACTCCTCCTGCTCCAGCTCCACTTCTATTCCACGG
AGAAAAAAATTGATTGTGTACAGAACAGTTTATGGAAACTAGCACCAGTCTACAGAAC
TGAACCATTTGTTGAAAATAAAGCAGCATTCAAGAACATGAAGCTGCTGGGTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTCTGCTCTTCTTGGTGTGAGCTGGTCTTGGATTG
TATGTCAAAAGGTATGTGAAGGCCTCCCTTTACAAACAAGAACATCAGCAGAACAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAACGGCAATGATAGCAACCTTAATGAGGAATCAAAGA
AAACTGATAAAACCCAGAACAGAGTCAAGAGTCAAGAACACTACCGTGCATGCCGGAA
GCTGAAGTTAGATGAGACAGAACATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC
TTACCCCTGCCAGCTGGGAAATCAAAGGGCAAAGAACCAAAGAACAGTCCACCCCTT
GGTCTCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAACATGC
CCTTCCTTATTGTAACCTGCTGGATCCTATCCTCCTACCTCCAAAGCTCCACGGCC
TTTCTAGCCTGGCTATGCTTAATAATATCCCACGGAGAACAGGAGTTGCAAAGTGC
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCTCTGGCTGTGAGGCTAGG
TGGGTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTACTGATTCCGCAGCTCAGAC
CCTTCCTCAGCTCTGAAAGAGAACACAGTATCCCACCTGACATGTCCTTGAGCCGGTA
AGAGCAAAGAACATGGCAGAAAAGTTAGCCCCGTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAGCTAAAATAAGAACATGAACAAAGCTGAGGATAACGACAGTACACT
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCGACTGCTGATATTCT
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAATTCTATTCTATTCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAATTGACATAGTAGAACGCTATCTGGGAAGCTATTCT
GTTTGATATTCTAGCTTACTTCAACTAATTCTTATTGCTGAGACTAATCTT
ATTCACTTCTCTAATATGGCAACCATTATAACCTTAATTATTATTAAACATACCTAAGAAG
TACATTGTTACCTCTATATACCAAAGCACATTAAAAGTGCCATTAAACAAATGTATCACTA
GCCCTCCTTTCCAACAAGAACGGACTGAGAGATGCAGAAATTGTCAGCAAAAAATTAA
AGCATTAGAAAATT

FIGURE 74

MARCFSLVLLTSIWTTRLLVQ GSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISP NPKCGKNGGVLIWKVPVSRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTI PAPTTTPP
APASTSIPRRKKLICVTEVF METSTMSTETEPFVENKA AFKN EAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKA FPTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTATTGGTGCACGACTTTACGATGG
CTCGCCCAACCTTACTACCTCTGTCGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA
ACTGCCGCCGCTCTGCCACGGCTGCCACCCAACCGGAAGACGGTAACCGTGTGACTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAAGCAACATTTCATGTTAGTAAAGTGGCAACACAAT
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACTAGAACGGACAAGAGGGTCACGGATTGTGGAGTTCTTGCCAA
TTGGTCTAATGACTGCCATTCCTATCTATGCTGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTGGAGGTGGATGTTGGACGCTACTGATGTTAGTACGGTAC
AAAGTGAGCACATCACCCCTACCAAGCAACTCCCTACCCCTGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTCG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGCCAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTTCAACCCCCACCACAGTGTCA
TGGGAAAACAAGAAGGATAAAGATCCTCACTTGGCAGTGCTCCTCTCGTCAATT
CCAGGCTCTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTCCCTTGG
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTAAAGAGGCATCTAGGGATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGTTCAAGCTGGCTAGTGTGTTACTGCTTAC
TCATAGGACGGAGGGGGAAATGGTTCCCTCAAGCTGGCTAGTGTGTTACTGCTTAC
AGCTATTAGACATCTCCATGGTTCTCCATGAAACTCTGTTGTTACTCATTCTTAG
TTGACCTGCACAGCTGGTTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAATTTCCTTCAAGGACTCTGCTTCTTAAGCCCTCTGGCTCGTTATGGTC
TTCATTAAAAGTATAAGCCTAACTTGTGCTAGTCCTAAGGAGAAACCTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAACCCCCCTATTGTGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTCCCTTGTGTTAGGACTTGGAGGAGAAATCCCTGGACTTCAC
TAACCCCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRKLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMF SKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRACKLSKAGDNI PEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGGGCCCCCGAGAGCTCTAGCCGTCAGGAGCTGCCCTGGGACGTTGCCCTG
GGGCCCTGGCCGGGTACCCCTGGCATGAGGAGATGGGCCTGTTGCTCCTGGTCCC
TTGCTCCTGCTGCCGGCTCTACGGACTGCCCTCTACAACGGCTTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGGAGACCCCTGTTCACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCTGGTCTCCCCGGCGTGTGCGTCAAATGGTGGAAAGCT
GTCGGAGAACGGGCCAGAGAACGGACGTGCTGGTGGCCATGGGCTGAGGCACCGCTCCT
TTGGGACTACCAAGGCCGCGTGCACCTGGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCGCTGGAGGACTATGGCGTTACCGCTGTGAGGTATTGACGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGTGTGGCTTCCCTTACAGTCCCCCA
ACGGCGCTACCAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCC
GTGGCCTCCTTGAGCAGCTCTCCGGGCTGGAGGAGGGCTGGACTGGTGCAACGCC
CTGGCTGCAGGATGCTACGGTCAGTACCCCATCATGTTGCCCGGCAGCCCTGCC
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACGCCCTGCC
GTATTCTGCTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCC
GACGCTGACAGAGGAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCC
AGCTCTTGCCGCTGGAAGTCCATGGCCTGGACCGCTGCGACGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCGTGGTTCACCGCATCCTAACTGTGGCCCCAGAGCCTGGG
CCGAAGCTTGCGCTCCCCGACCCGAGAGCGCTGTACGGTGT
ACTAGGACCTGGGCCCTCCCTGCCGCATTCCCTCACTGGCTGT
CGTTTCCCTGTGGTTGGAGCCATTAACTGTTTATACTTCTCAATTAA
TTAACATTTTTACTATTTTGTAAGCAAACAGAACCC
GATGCCCACTCCAGGAATCATGCTTGCTCCCTGGCCATTGCGGTT
GAGGTTCCCCGCATCCAGGCTGGCTCCCTCCCTTAAGGAGGTTGG
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGCATGGTGG
CACAGTTCTCCCTGTAAGCCGCTGACCC
CACCTCTACTCTCTGTGAAGCCGCTGACCC
GAGGAGAAGAAACTCC
TCCCTCTCGGTTCAAAGAATCTGTTGTCATTGTTCT
GGAGGGGCCCTCAGGTGTGTACTTG
GGACAATAAATGGTGT
GACTGCC
AAAA
AAAA

FIGURE 78

MGLLLVPLLLPGSYGLPYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFVQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEELDWNCAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGP
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGACCGATGATGTGGCACCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGCCAGGGAAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGCCCTGAGCGACGCTCCCCATGATGACGCCACGGAA
CTTCCAGTACGACCATGAGGCTTCCTGGACGGAAAGTGGCAAGGAATTGACCAACTCA
CCCCAGAGGAAAGCCAGGCCGTCTGGGCGGATCGTGGACCGCATGGACCGCGGGGAC
GGCGACGGCTGGGTGTCGCTGGCCGAGCTCGCGCGTGGATCGCGCACACGACAGCGCA
CATACGGGACTCGGTGAGCGCGCCTGGACACGTACGACACGGACCGCGACGGCGTGTGG
GTTGGGAGGAGCTCGCAACGCCACCTATGCCACTACCGCCGGTGAAGAAATTGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTGGACGAGCGGCGTTCCGGTGGC
CGACCAGGATGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTCCTGCACCCGAGG
AGTCCCTCACATCGGGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGGGATCTGTACTCAGCCGAGCCTGGGAGGA
GGAGCCGGCGTGGTGCAGACGGAGAGGCAGCAGTCCGGACTTCCGGATCTGAACAAGG
ATGGGCACCTGGATGGAGTGGACTGGGACTGGGTGCTGCCCTGCCAGGACAGCCC
CTGGTGGAAAGCCAACCACCTGCTGCACGAGAGCAGACGGACAAGGATGGCGGCTGAGCAA
AGCGGAAATCCTGGTAATTGAAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACACGATGAGCTTGAGCACCGCCACCTGCCACAGCCTCAGAGGCCCG
CACAATGACCGGAGGAGGGCCGCTGGTCTGGCCCTCCCTGTCCAGGCCAGGCGAGGAG
GCAGATGCAGTCCAGGCATCCTCCTGCCCTGGCTCTCAGGGACCCCTGGTCGGCTTC
TGTCCCTGTCACACCCCAACCCAGGGAGGGCTGTCATAGTCCCAGAGGATAAGCAATAC
CTATTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTGCCAGGAAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCAAATCTGAGCCTCCACCATAGACTGAAACTCCCT
GGCCCCAGCCCTCTCCTGCCCTGGCCTGGACACCTCCTCTGCCAGGAGGAATAA
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSPDAGPHQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDWVSLAERAWIAHTQQRHIRDSVSAAWDT
YDTDGRVGEELRNATYGHYAPGEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKDGHLDGSEVGHVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTGCCCTCCGCACTCGGGCGCAGCCGGTGGATCTGAGCAGGTGC GGAGCCCCGG
GCGGCGGGCGCGGGTGCAGGGGATCCCTGACGCCTCTGTCCTGTTCTTGCGCTCCCAG
CCTGTCGTCGTCGTTGGCGCCCCCGCCTCCCGCGGTGCGGGGTTGCACACCGATCCTG
GGCTTCGCTCGATTGCCCGAGGCCCTCCCAGACCTAGAGGGCGCTGGCCTGGAGCAG
CGGGTCGTCGTCGTCCTCTCCCTGCGCCGCCCGGGATCCGAAGGGTGC GGGGCTCT
GAGGAGGTGACGCGCGGGCCTCCGCACCCCTGGCCTGCCGCATTCTCCCTCTCCCAG
GTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCCGCTCTGGCCTCGGTGTG
TGTCTGCTGCTGCCGGGCGCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATG
TTTACCAAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGCTGCC
CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTCTGTATCGAGCATATGTGGG
GCTGCTGTCCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC
TGGTCGAGAAA ACTATTCCCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGAT
GGTCTGCTCTTCACAGTAACTAAAGGCAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAA ACTGG
CAATAAAGATTGTAAGCAGACATTGCATTCTGATTGATGGAAGCTTAATATTGGCAGC
GCCGATTAAATTACAGAAGAATTGTTGGAAAAGTGGCTCTAACATGTTGGAAATTGGAACA
GAAGGACCACATGTGGCCTTGTCAAGCCAGTGAACATCCAAAATAGAATTACTTGAA
AAACTTACATCAGCAAAGATGTTGTTGCCATAAAGGAAGTAGGTTAGGTTAGGGGTA
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGGTATTATTGATGTTGGCCTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTGGTGTCAATGTATTAGTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGATGTTCAGGATGTCACATTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTCTTACACATGCCCAACTGGTTGGCACCAAAAATACGTAAA
GCCTCTGGTACAGAACGCTGTGCACTCATGAACAAATGATGTCAGCAAGACCTGTTATAACT
CAGTGAACATTGCCTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCCTC
ATGCTTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTCCAAGAT
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCACTGACTATAGCACCA
AAGAGAATGTCCTAGCTGTCACTAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT
GATGCCATTCTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCCTAGTAATTGTCACAGATGGGCAGTCCTATGATGATGTCAGGCTTGCGCTGAGCTGCTG
CACATGATGCAGGAATCACTATCTCTGTGGTGTGGCTGGCACCTCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTACGCTTCTCACAGAGAGTTCAACAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGTTAGAGATTCTTAGAATCCCAGCAAT
AATGGTAACATTGACAAC TGAAAGAAAAAGTACAAGGGGATCCAGTGTGAAATTGTATT
CTCATAATACTGAAATGCTTCTGATGTCAGGAGTCAACATGAGATACAAAATATTAAGTATGTCAAC
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCTCTGGTTACAATTACAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTCTAGAAAACCTCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEAAPIAITCFTRGLDIRKEKADVLCPGGCPLLEFSVY
GNIVYASVSSICGAAVHRGVI SNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTP EKKTGNKDKCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNNGFFSYHMPNWF GTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLA
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCCGCGCTCCGCACCCGCGGCCGCCACCGCGCCGCTCCGCATCTGCACCCGAGCCC
GGCAGGCTCCGGCGGGAGCGAGCAGATCCAGTCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCG
GGGGGGCGGCTGCGGGCGCAGAGCGGAGAT**G**CAGCGGCTTGGGCCACCCCTGCTGCGCTGC
TGCTGGCGGGCGGCGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTC
AAGCCCGGCCGGCTCTCAGCTACCCGAGGAGGAGGCCACCCCTCAATGAGATGTTCCGCGA
GGTTGAGGAAGCTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACACTACCTCCCAGCTAT
CACAATGAGACCAACACAGACACGAAGGTTGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGAGACAGTGAGTGCAGTGACATCATCGACGAGGACTGTGGGCCAGC
ATGTA**T**GTGCCAGTTGCCAGCTTCAAGTACACCTGCCAGCCATGCCGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCAGTGAGGAGACAGCTGTGTCTGGGTCACTGCACCAAAA
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAAACCAGAGGGACTGCCAGCCGGGCTG
TGCTGTGCCTCCAGAGAGGGCTGCTGTTCCCTGTGTCACACCCCTGCCGTGGAGGGCGA
GCTTTGCCATGACCCGCCAGCGGCTTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG
GAGCCTGGGACCGATGCCCTTGTGCCAGTGGCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTTGCCAGCTTCATGGAGGAGGTGCCAGGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGTGCCGCT
GCACTGCTGGAGGGGAAGAGATT**T**AGATCTGACCGAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTCCCCAGGTGTGCTTAGGCGTGGCTGACCAGGCTTCTCCTACA
TCTTCTTCCCAGTAAGTTCCCTCTGGCTGACAGCATGAGGTGTTGTGCATTGTTAGC
TCCCCCAGGCTGTTCTCAGGCTCACAGTCTGGTGTCTGGAGAGTCAGGCAGGGTTAAC
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACAGTTGGCAG
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGGAAACAATGTGG
AGTCTCCCTCTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAAACATCAA
CCTGGAAAAATGCAACAAATGAATTTCACCGCAGTTCTTCCATGGCATAGGTAAGCTG
TGCCTTCAGCTGTTGAGATGAAATGTTCTGTTCACCCGCATTACATGTGTTATTCATCC
AGCAGTGTGCTCAGCTCTACCTCTGCCAGGGCAGCATTTCATATCCAAGAGATCAATT
CCTCTCTCAGCACAGCCTGGGGAGGGGTCTTGTCTCCTCGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACAGCAGCAGTTCAT
CTGGTTGTGACTCTAAGCTCAGTGCTCTCCACTACCCACACCAGCCTGGTGCCACCAA
AAGTGTCCCCAAAAGGAAGGAGAATGGGATTTTCTTGAGGCATGCACATCTGAAATTAG
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGCAGCCGTCTTCTAATGAAGACAATGATATTGACACTGTCCCTTTGGCAGT
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATAAGGTTAACCTGCAGAAACA
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTGCAAACACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGAAACATGGTT
GTAATATGCACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTGACACTCCAGAGTTCTAAAGTTAAAGTTGCACATGATTGTA
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTTGCATTAGAAATCAAGC
ATAAAACTCACTCAACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEAEAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGIELLPREVPDEYEV
GSFMEEVVRQELEDLERSLTEEMALGEPAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGGCTGGGAGGAAAGAGGTAAGAAGAAGGTTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCTG
AAGATAACAATAATTTCAGCCCCATCCACTCTCCTTCCCTCCAAACACACATGTGCATGTACACACACACATACA
CACACATACACCTTCCTCTCCTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCA TAGAAAAGGACAC
TAAAGCCTTAAGGACAGGGCTGGCATTACCTCTGCAGCTCTTGAGTGTGAGTCAAAAAAACATGGGAGGG
CCAGGCACGGTGACTCACACCTGTAATCCCAGCATTTGGAGACCGAGGTGAGCAGATCACTTGAGGTCAAGGAG
TTCGAGACCAGGCTGGCCAACATGGAGAAACCCCCATCTACTAAAAAATACAAAAATTAGCCAGGAGTGGTGGC
AGGTGCTGTATCCCAGCTCAGGTGGCTGAGCAGGAGAATCGCTTGAATCCAGGAGGGAGGATGCCAGT
CAGCTGAGTGACCGCTGCACTCCAGCCTGGGTGACAGAAATGAGACTCTGTCTCAAACAAACACAGGGAGGA
GGGTAGATACTGCTTCTGCAACCTCTTAACCTCTGCATCCTCTTCCAGGGCTGCCCTGATGGGCCCTG
GCAATGACTGAGCAGGCCAGGCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGA
GCCCGTAGTAACTGCTTCTGCAACCTCTTAACCTCTGCATCCTCTTCCAGGGCTGCCCTGACCCCTGCAAAACACA
AAGAGCAGGACTCCAGACTCTCCTTGTGAATGGTCCCCCTGCCACTGAGCTCCACCATGAGGCTTCTCGTGGCCCC
ACTCTTGCTAGCTGGGTGGCTGGTGCCTGCCACTGCCACTGTGCCGTGGTACCCCTGGCATGTTCCCTGCC
GTGTGCTGCCAGATCCGGCCCTGGTATACGCCCGCTGTCCTACCGCGAGGCTACCAACTGTGGACTGCAATGA
CCTATTCTGACGGCAGTCCCCCGGCACTCCCCCGCAGGCACACAGACCCCTGTCCTGAGAGCAACAGCATTGT
CCGTGTGGACCAGAGTGA GCTGGGCTACCTGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTGG
TGCCCGAGACTGTGATTTCATGCCCTGCCAGCTGCTGAGCCTGCACCTAGAGGAGAACAGCTGACCGGCT
GGAGGACCACAGCTTGCAAGGCTGGCAGCTACAGGAACCTATCTCAACCACAAACCAGCTCACCGCATCG
CCCCAGGGCTTTCTGGCTCAGCAAATTGCTGCCGCTGCACCTCAACTCCAACCTCTGAGGGCCATTGACAG
CCGCTGGTTTGAATGCTGCCAATTGGAGATACTCATGATTGGGGCAACAGGTA GATGCCATCCTGGACAT
GAACATTCCGGCCCTGGCAACCTGCGTAGCCTGGTAGCAGGATGAACCTGCCGGAGATCTCGACTATGC
CCTGGAGGGCTGCAAAGGCTGGAGAGCCTCTATGACAACCAAGCTGCCCGGGTGCCAGGCGGGCACT
GGAACAGGTGCCGGCTCAAGTCTCTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCGGGGACTTGC
CAACATGCTGACCTTAAGGAGCTGGGACTGAACAAACATGGAGGAGCTGGTCTCCATCGACAAGTTGCC
GAACCTCCCCGAGCTGACCAAGCTGGACATCCAATAACCCACGGCTGTCTTCTATCCACCCCCCGCCTTCA
CCACCTGCCCTAGATGGAGACCCCTCATGCTCAACAACAGCTCTAGTCCCTGCACCCAGCAGACGGTGGAGTC
CCTGCCCAACCTGCAAGGAGTTAGGTCTCACGCCAACCCATCCGCTGTGACTGTGTCATCCGCTGGCCAATGC
CACGGGCAACCGTGTCCGTTCATCGAGCCGAATCCACCCCTGTGCGGAGCTCCGACCGCCTCC
GGTCCGTGAGGTGCCCTTCCGGAGATGACGGACACTGTTGCCCTCATCTCCCCACAGAACGCTTCCCC
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCAATTGCCGGCACTGCCGAACCCGAACCCGAGATCTACTG
GGTCACCTCAGCTGGCTTCGACTGACACCTGCCATGCAGGCAAGGAGGTACGGGTACCCCGAGGGAC
GGAGCTGGAGGGTACAGCAGAAAGAGGCAAGGCTATACACCTGTGTCGCCAGAACCTGGTGGGGCTGACAC
TAAGACGGTTAGTGTGGTTGTGGGCCGTGCTCTCCTCCAGCCAGGCAAGGGAGAAGGACAGGGGCTGGAGCTCG
GGTGCAGGAGACCCACCCCTATCACATCCTGTATCTGGGTCAACCCACCCAACAGTGTCCACCAACCTCAC
CTGGTCCAGTGCCTCCCTCCGCCAGGGGCCACAGCTGGCCCTGCCTGGGGAAACCCACAGCTA
CAACATTACCCGCTCTCAGGCCACGGAGTACTGGGCTGCCATGCAAGTGGCCTTGTGATGCCACACCA
GTTGGCTTGTATGGGCCAGGACAAAGAGGCCACTCTTGTGCCACAGGCCTAGGGATGTCCTGGGCTCAT
TGCCATCCTGGCTCTGCTGCTCTGCCAGCTGGCTAGCGGCCACCTTGGCACAGGCCAACCCAGGAA
GGGTGTGGGTGGAGGCGGCCCTCCAGCTGGCTTCTGGGCTGGAGTGCCCTCTGTCCGGTTGT
GTCTGCTCCCTCGTCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAGACACTGTTGCC
ACCATTGTCTAAAATTCTTGAAGCTCAGCTGTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTACAAA
AGAGAACAGTCTGGGCCAGATGCCCTGCCAGAAAGGGACATGGACCCACGTGCTGAGGCCCTGGCAGCTGGC
CAAGACAGATGGGGCTTGTGGCCCTGGGGTCTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCTAGGGTCA
CCTCTGCTGCCATTCTGAGGAACATCTCCAAGGAACAGGGAGGACTTTGGCTAGAGCCTCTGCC
CTCTCTGCCAGAGGCTCTGGCCCTGGCTTGTGCTCTGTGCTCTGCCAGGGCTGAAGGAGGCCACTCC
TCTTCTCTGTACAGTCTCAGTTGCTTGTGCTCTGTGCTCTGCCAGGGCTGAAGGAGGCCACTCC
CTCGGGGGCTGCCCTCAATGTGGAGTGACCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCC
CGCCTCATCTCAGCAGCCTGGCTGGCATTCCGAAGCTGACTTTCTATAGGCAATTGTACCTTGTGGAGAA
ATGTGTCACCTCCCCAACCGATTCACTCTTCTCTGTAAAAAATAAAATAACAATAAAA
AAAA

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDNDLFLTA
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQEELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMDNFRPLANLRSILVLAGMNLREISDYALEGLQSLSESLSFYDNO
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNPRLSFIHPRAFHHLQPQMELMLNNNALSALHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT
CVAQNLVGADEKTVSVVGRALLQPGRDEGQGLELRVQETHPYHILLSWTPPNTVSTNLTW
SSASSLRGQQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLAAHLGTGQPRKGVGGRPLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGGCCAAGGCGCTGGTGTGAGAAGGTGAAGAAGTCCGGACCCATGTGGAGGAGGGGACATTGTGTACCGCC
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTGAGCTGGACTGCACCGTGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCCACCC
CCTGGCCACACTCTTCAGATCCTGGCGTCCTTCTACATCAGCTAGTCATCTTCTACGGCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCTTCATGCTGCACCTCATGACCAATACGACCCGCTACTCCAA
GCGCTTCGCCGTCTCCTGCGAGGTGAGTGAGAACAAAGCTGCGGAGCTGAACCTCAACAACGAGTGGAGCCT
GGACAAGCTCCGGCAGGGCTACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTCATGCTCAGTGGCAT
CCCTGACACTGTGTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCGCC
CAGCATTGCCAGCTCACGGCCTCAAGGAGCTGTTGAGCTTACACACAGCGGCAAGATTGAAAGCGCTGCGCT
GGCCTTCCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTACCGACATCAAGGAGATCCGCTGTTGAGCTA
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGCAACCTGAGCGGGAGAACAAACCGTACATCGTCATCGA
CGGGCTGCGGGAGCTCAAACGCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGTGGTCAC
AGATGTGGGCGTGCACCTGCAAGAGCTGTCATCAACAAATGAGGGCACCAAGCTCATGTCCTCAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTCAGCCT
CCACAACTCAGGAGATTGACCTCAAGGACAACAAACCTCAAGGACCATCGAGGGAGATCATGCTTCAGCACCT
GCACCCGCTCACCTGCTTAAGCTGTTGACCAACACATGCCCTACATCCCCATCCAGATCGGCAACCTCACCAA
CCTGGAGCGCTCTACCTGAAACCGCAACAAGATCGAGAGAAGATCCCCACCCAGCTTCTACTGCGCGAAGCTGCG
CTACCTGGACCTCAGCCACAACAAACCTGACCTTCTCCCTGCGACATCGGCCCTCTGCGACAACCTCCAGAACCT
AGCCATCACGGCAACCGGATCGAGACGCTCCCTCGGAGCTTCCAGTGCAGGAGCTGGGGCCCTGCGCACCT
GGGCAACAACGTGTCGAGTCAGTCACTGCCCTCCAGGGTGGCGAGCTGACCAACCTGAGCGAGATCGAGCTGGGGG
CAACCGGCTGGAGTGCCTGCTGTGGAGCTGGCGAGTGCCTACTGCTCAAGCGCAGGGCTTGGTGGAGGAGA
GGACACTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGTGTGGAGGGCTGACAAAGGAGCAGGCTTGAGCAG
GCCGGCCAGCACGCAAGCAGCAGGACCGCTGCCAGTCAGTCTCAGGCCGGAGGGCTAGCTTCTCCAG
AACTCCGGACAGCCAGGACAGCCTCGGGCTGGCAGGAGCCTGGGGCCTTGTGAGTCAGGCCAGAGCAGA
GGACAGTATCTGTTGGGCTGGCCCTTTCTCCCTGAGACTCACGCCCCCAGGGCAAGTGTGTTGGAGGAG
AGCAAGTCTCAAGAGCCAGTATTGGATAATCAGGGCTCCTCCCTGGAGGCCAGCTGCCCCAGGGCTGAG
CTGCCACCAGAGGTCTGGGACCCCTCACTTAGTTCTGGTATTATTCTCCATCTCCACCTCCTCATCC
AGATAACTTACATTCCAAGAAAGTTCAGCCAGATGGAAGGTGTCAGGGAAAGGTGGCTGCCCTTCCC
TTGTCTTATTAGCGATGCCCGGGCATTAAACACCCACCTGGACTTCAGCAGAGTGGCCGGGGGAACCA
CCATGGGACGGTCACCCAGCAGTGCCTGGCTCTCAGTTTGTGGAGTTAGTTTTTTTTTTTTAAATCAA
AAACAATTTTTAAAAAAAGCTTGAAATGGATGGTTGGTATTAAAAGAAAAAAACTAAAAAAA
AAAAGACACTAACGGCCAGTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTGAGCAAAGCAGCCAGACGT
TGAACGTGTTCTTCCCTGGGCGCAGGGTGAGGGGTGCTTCCGATCTGGTGTGACCTTGGTCAGGAGTT
CTATTTGTTCTGGGAGGGAGGTTTTTTGTTGTTTTGGGTTTTGGTGTCTTGTGTTCTTCTCCTCC
ATGTCCTGGCAGGCACTCATTCTGCGCTGCGGCCAGAGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGCTGGCTAATCCCCGGATGAACGGTCTCCATTGCCACCTCCCTCTCGCTGCCCTGCCCTCTCCA
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTTCGCCAGACTTGTGTTCCCTGCCACCTCTGGCTGCCATGGGTGTT
CCAGTGCCACCGCTGGCCTCCGCTGCTCCATCAGGCCCTGCGCACCTGGCTTCTGAGAACAGAGCAGACACTTA
GAGGCTGGCTGGGAATGGGGAGGTGCGGCGAGGGCTGGTCTTCAAGGCCGTTCCGGTCTGCCCTGGCGC
CTGGAGTGCACACAGCCAGTGGCAGCTGGCTGGAGCCAACCTGCTTGTGACACTCGGGTCTCCCGACCTT
AGAAGGGTCCCCGCCCTAGATCAATCACGTGGACACTAAGGCACGTTTAGAGTCTCTGCTTAAATGATTATGT
CCATCCGTCTGTCGTCCTTGTGTTCTGCGCTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGAAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAA
ATCTATAACAGAAAAAAAAAAAAAA

FIGURE 88

MRQTIIKVIKFILIIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQLNLNNNEWTLDKLRQRLTKNAQDKLELHLFMLSGIPDTVFSDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFDTIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHGNVLQSLPSRVGELETNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCAATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCCTATT
GTGGATAATCCC GTGGCACTGGTT CAGTT ATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
AATTCCAGACAGTTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTATAAGGCCATTCA CGCAGGGACC ATCAAGTGC AAC TTGCGGGG
TGCCTGGGTGATT CCTGGATCTCCCTGTTGATT CGGTGCTCTCCTGGGACCTTACCTGT
ACAGCATGTC TCTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTGCAAGAGCAAGTA
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGGCCACCTAGTTGTCTTGTCAAGC
CACGTGAGACACCTACAACGAGATGCCCTAACGCCAGCTCATGAATGCCCATCAGAAAGAA
GCTAAAATTATTCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATAACCATGGGTCAAGGAGGC
GGTGGCGAAACTGAAGTGGCCAGAACTGCCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCC
ACAGTGAACCTAAATCTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTT
TACTGGATTCTGAAAGCTGGTCAATGGTTCTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTACTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGC
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTCTGACCAGCTCTGCAGAGGATAAAATCATTGTCT
GGAGGCAATTGGAAATTATTCTGCTTAAAAAAACCTAAGATTTTAAAAAATTGAT
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPPLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELGKAEMIIEQNTDGVNFYNILTKSTPTSTMESLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQOE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCAGGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTGCGCATTGAGGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCGCACTGCTTGAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCACCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCATCTGTCTCCAG
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCAGTGCATCTCCCCACACCCTCCAGGAAGTTCAGGTGCCATCATAAACAA
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG
GTTTGTGCTGGCAACGCCAACGGCGGAAGGATGCCTGCTCGGTGACTCAGGTGGACCCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCGGTGTCTACACCAATATCAGCCACCACCTTGAGTGGATCCAGAAG
CTGATGGCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTCCCTCT
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTTCTCTGTCTTGTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLLALLLARAGLRKPESQEAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW
DSHVCGVSLLSHRWALTAAHCFETYSDSLDPGWMQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEJVQVIAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWGVGCGRPVRPGVYTNIHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCACCGCGTCCGGACCGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCTAGGGCT
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCCAGGCCGACCAGCGAGGACGC
TGCCCCCAGGCTGGGTGCCCCCTGGCGGTGCGGACCCCTGAGGAAGAGCTGAGTCACCTT
GCCCTGAGACAGCAGAATGTGAAAGACTCTCGGAGCTGGTGCAGGCTGTGTCGGATCCCAG
CTCTCCTCAATACGAAAATACCTGACCCCTAGAGAATGTGGCTATCTGGTGGCCATTCT
CACTGACCCCTCCACACGGTGCAAAATGGCTCTGGCAGCCGGAGCCCAGAAGTGCCATTCT
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTCATCACTATGTGGGAGGACCTACGGAAACCATGTTGTAAGGTCCCCAC
ATCCCTACCAGCTTCCACAGGCCTGGCCCCCATGTGGACTTTGTGGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGCAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGTAACCCCCTGTGATCCGTAAGCGATACAACCTGACCTACAAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCTGGAGCAGTATTCCATGAC
TCAGACCTGGCTCAGTTCATGGCCTCTCGGTGGCAACTTGACATCAGGCATCAGTAGC
CCGTGTGGTTGGACAACAGGGCCGGGCCGGGATTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGCTGGTGCACATCTCACCTGGCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTTCTGCAGTGGCTATGCTGTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGGCCCTACATCCAGCGGGTCA
ACACTGAGCTCATGAAGGCTGCCCTGGGTCTCACCTGCTTGCCTCAGGTGACAGT
GGGGCCGGGTGTTGGTCTGTCTCTGGAAAGACACCAGTTCCGCCCTACCTTCCCTGCCCTCAG
CCCCTATGTCACCACAGTGGAGGCACATCCTCCAGGAACCTTCCTCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCACGGCCTTCATACCAGGAG
GAAGCTGTAACGAAGTTCTGAGCTTAGCCCCCACCTGCCACCATCCAGTTACTTCATGC
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACCTTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGCCCATTCATGGGTGTCGGAACCTCGGCCTCTACTCCAGTGGTTGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCTCTGGCTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGCAGGTCTTTGATGTAACCGTGGCTGCCATGAGTCCTGTC
TGGATGAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGCTGGATCCTGTAACAGGC
TGGGGAACACCAACTCCCAGTTGCTGAAGACTCTACTCAACCCCTGACCCTTCCTATC
AGGAGAGATGGCTTGTCCCCCTGCCCTGAAGCTGGCAGTTCACTCCCTTATTCTGCCCTGTTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA
TGCTGTGAGCTTGACTTCAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCCTAGATTCTCAATAAGATGCTGTAACTAGCATTTTGAAATGCCCTCCCTCCGC
ATCTCATCTTCTCTTCAATCAGGCTTTCAAAGGGTTGTATACAGACTCTGTGCACTA
TTTCACTGATATTCAATTCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT
TTCCTACCTGACATCCAGAAACAATGGCCTCCAGTGCATACTCTCAATCTTGTGTTATG
GCCTTCCATCATAGTTGCCACTCCCTCTCCTACTTAGCTCCAGGTCTTAACCTCTG
ACTACTCTTGTCTTCCCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTG
TCCATTGTAGATTTGCTCTCAGTTACTCATTGTCCCCCTGGAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATAACCTCAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHYYVGGPTETHVRSRPHYQLPQALAPHVDFVGGLHRFPPSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSDVGSCTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLFASGDGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDDEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GCCGCGCGCTCTCTCCGGGCCACACCTGTCTGAGCGCGCAGCGAGCCGGCCGGG
GGGCTGCTCGCGCGAACAGTGTCGGCATGGCAGGGATTCCAGGGCTCCTCTTCTC
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTTG
GCCTGCATACCGCCTCCCTGCGTCTGCCCTAGTCTACCCCTAATTAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCAGTGTCTATAAGGAACT
CCACTGCCCACCTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGTCTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAAAGGACTTCCTGCTCAACTACCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGCACCCGGTGGCAGAGAACGCTGCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAACGCTTGAGTGGCTTCCTAAAGCCC
AAGTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCGAGCAGATGAA
ATTCAGTGGATCCGGTGAAACGCACCCATGTGCCAAGGGTGGATCAAGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCTGGAACTAAAAAGCCCACAAGAGAAAA
TTTATGAAGATTGGGTGAGCCCTCTGCTAAGCAGCTGCCAGGGGCCAGAATTCACTTCTC
TGGTTATGACAATGACCGACCAGGCAATTGGTGTATCGCTCTGTGACGTCAAAGACGAGA
CCTATGACTTGTCTACCAGCAATGCGATGCCAGCCAGGGGCCAGGGCTGGCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAACGAGCGAAAAATTATTGGCATTTCAGG
GCACCAAGTGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTAGAACACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG
TGACACAGTGTCCCTCTGGCAGCAATTAAAGGGTCTCATGTTCTTATTTAGGAGAGGCC
AAATTGTTTGTCTGGCGACACGTGTGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTACCTATTCTACAATTGCAAGATGACTGGCTTACTATTGAAAAGTGT
GTTTGTGTATCATATCATATCATTAAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAACTGATTGGGCAATGAGGAATATTGACAATTAAAGTTAATCTCACGTTTG
CAAACTTGATTTCATCTGAACCTGTTCAAAGATTATTAATATTAAATATTGGCATA
CAAGAGATATGAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLQPSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRD
SGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHV
LTAACIH
DGKTYVK
TQKLRVGFLKP
KF
KG
G
R
G
A
N
D
S
T
S
A
M
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E
Q
M
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F
Q
W
I
R
V
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H
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I
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G
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A
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G
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Y
D
Y
A
L
L
E
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K
R
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F
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V
S
P
P
A
K
Q
L
P
G
G
R
I
H
F
S
G
Y
D
N
D
R
P
G
N
L
V
Y
R
F
C
D
V
K
D
E
T
Y
D
L
L
Y
Q
Q
C
D
A
Q
P
G
A
S
G
S
G
V
Y
V
R
M
W
K
R
Q
Q
Q
K
W
E
R
K
I
I
G
I
F
S
G
H
Q
W
V
D
M
N
G
S
P
Q
D
F
N
V
A
V
R
I
T
P
L
K
Y
A
Q
I
C
Y
W
I
K
G
N
Y
L
D
C
R
E
G

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCACCAGCCATGGTGGTT
CTGGAGCGCCCCAGCCCTGGGTGGGGCTGTCTCGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGCGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTGCTCACCAAGCCGCTGGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACTGTTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGAACCCCTGGCTCTGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCCCTGTGTATTCTGGAAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGCCTGCCCATCTGCCTACCTGATGCCCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTCCCTTGC
CCCACCCCTCAGACCCTGCAGAAGCTGAAGGTT CCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCGGCATCATCAGCTGGGGCGAGGGCTGTGCCAGCGAACAGGCC
GGGGTCTACATCAGCCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTCAAGGGGTGCA
GCTCCCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCC
CCGGCGCTCCTAGGGCGCAGCGGGACCGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGCGGCCTCGGGCGGTTCCCGCCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCGGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGCCAACGGCCTCATGTCCCCGCCAC
GACTTCCGGCCCCGCCCGGGCCCCAGCGCTTTGTATATAATGTTAATGATTATT
AGGTATTTGTAACCCTGCCCACATATCTTATTTATTCCCTCCAATTCAATAATTATT
CTCCAAAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAHCFKDNLNKPYLFVLLGAWQLGNPGSRSQKVGVVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGII SWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTCTGATGCTCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCCTTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGCCAC
AACAAAGGAGCGCGGGCGCCGGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGGCCCGCACCT
GCAGCCCAGGCCAGATGTGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC
GGCTGTGGTCCCACCTCTGTGAGAAAGCTCCAGGGTTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC
CGTGCTCCCAATGTCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTGCCCTACCTGGTAAC TGAGGCCCATCCTCCGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTCTTCAGCAACGGGATTCCGGCTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCCTGTGGAAACCCAGGCC
CCAACTTCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTGCGTAAC
AACTGAGGTCCCTTCCATTTGGCAGCTCACAGCCTGCCCTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTCCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGCAAG
GGAACCTCCTACCCCATGCCAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCAGTG
AGGTCTTGGCCTCAGTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCGTCCCTGCCAGGTGCAGAGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGCCCTGGCATGTGTGGGCCCTCCCTGGGA
CTACTGCTCCTGCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCAACTCAAAGGG
TGAAGAGGTAGCTGTCCTCTGTCACTTCCCCACCCCTGTCCCCAGGCCCTAAACAAGATA
CTTCTGGTTAAGGCCCTCCGAAGGGAAAGGCTACGGGCATGTGCCCTCATCACACCCTCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCACACCTCCTGCCCTCCCTGCCAGTCCTGGGCTGGGAGGATTGAGGGAGCT
CACTGCCTACCTGGCCTGGGCTGCTGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG
TGTAGCTGGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTTC
TTTGAGTGGGGAGGCAGGGACGGGAAGGAAAGTAACCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPASDMLHMRWDEE
LAAFAKAYARQCVCWGHNKERGRRGENLFAITDEGMVDPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPyQEGETPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPYLTVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAHSILPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSMDPKMSLTGARELLPHAQEEAEAEALPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAECPDKPSVV
SGLNSGPVGVWGPPLLGLLLPPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACGTGAGTCAGGCTTTCATTGGGAAGCCCCCTCAACAGAACCGGTCACTCCAAAGTTATGGTGGACGT
ACTTCTGTTCTCCCTTGCTTTACATTAGCAGACGGGACTTAAGTCACAACAGATTATCTTCAT
CAAGGCAAGTCCATGAGCCACCTCAAAGCCTCGAGAAGTGAACAAACAAATGAATTGGAGACCATTCC
AAATCTGGGACCAAGTCTCGGCAAATATTACACTTCTCTCCTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
ACATCTGAAAGAGTTCACTCCCTGAAACTTTGGACCTAGCAGAACAAATATTCAAGAGCTCCAAACTGCATT
TCCAGCCCTACAGCTCAAATATCTGTATCTCACAGAACCGAGTCACATCAATGAAACCTGGGTATTTGACAA
TTTGGCCAACACACTCCTGTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAAGATGTTAAACT
GCCCAACTGCAACATCTGAATTGAACCGAAACAAGATTTAAAGTAGATGGACTGACATTCCAAGGCCTGG
TGCTCTGAAAGTCTGAAATGCAAAGAACGGAGTAACGAAACTATGGATGGAGCTTTGGGGCTGAGCAA
CATGAAATTTGCACTGGACCTAACAAACCTAACAGAGATTACAAAGGCTGGCTTACGGCTTGCTGATGCT
GCAGGAACCTCATCTCAGCCAAATGCCATCACAGGATCAGCCCTGATGCCCTGGAGTCTGCCAGAACGCTCAG
TGAGCTGGACCTAACCTCAACTTCAAGGTTAGATGATTCAAGCTTCTGGCTAACGTTACTAAATAC
ACTGCACATTGAGAACAAACAGTCAGCTACATTGCTGATTGCTTCCGGGGCTTCCAGTTAAAGACTTT
GGATCTGAAAGAACATGAAATTCTGGACTATTGAGACATGAATGGTCTTCTGGGATGCTGATGCT
GCGACTGATACTCCAAGGAAATCGGATCCCTTACTAAAGGCTTCACTGGTTGGATGCTTGGAGCA
TCTAGACCTGAGTGAACACGCAATCATGCTTACAAGGCAATGCATTTCACAATGAAGAAACTGCAACAAATT
GCATTAAATACATCAAGCTTTGTGCAATTGCCCAGCTAAAGGCTCCACAGTGGGGGGGAAACAAACCTT
TCAGAGCTTGTAATGCCAGTTGCTGATTGCCATCCTCAGCTGCTAAAGGAGAACAGCATTGCTGTTAGCCCAGA
TGGCTTGTGAGTATTCCAAACCCAGATCACGGTCAGCCAGAACACAGTCGGCAATAAAAGGTT
CAATTGAGTTCATCTGCTCAGTCAGCAGTCAGTGAATTCCCAATGACTTTGCTTGGAAAAAGACAATGA
ACTACTGCATGATGCTGAAATGAAAATTATGCAACACCTCCGGGCCAAGGTGGCGAGGTGATGGAGTATACCAC
CATCCTCGGCTGCGAGGTGAAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCAATCATTGGTTC
ATCCTACTCTGCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCAACAGACCCCCATGGATCTCACCAT
CCGAGCTGGGGCATGGCACGCTGGAGTGTGCTGCTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAACGA
TGGGGGACAGACTTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCAGGATGACGTGTTCTTATCGT
GGATGTGAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTCAGGAAGTATTGCAAATGC
AACTCTGACTGCTCTAGAAACACCATCATTGCGGCCACTGTTGGACCGAATGTAACCAAGGGAGAACAGC
CGTCCTACAGTGCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACCTGGACCAAAGATGATGCCATTGGTGG
AACCGAGAGGCACTTTTGCAAGCAGGCAATCAGCTCTGATTATTGAGTCTAGATGTCAGTGTGCTGGAA
ATACACATGTGAGATGCTAACACCCCTGGCACTGAGAGGAAACGTGCGCCTCAGTGATCCCCACTCCAAC
CTGCGACTCCCCCTCAGATGACGCCACTCGTAGACGATGACGGATGGGCCACTGTTGGCTGCTGATCATAGC
CGTGGTTGCTGTTGGGACGCTACTCGTGTGGGTCATCATACACACAAAGGGGGAGGAATGAAGA
TTGCAGCATTACCAACACAGATGAGACCAACTTGCAGCAGATATTCTAGTTATTGTCATCTCAGGGAACTGTT
AGCTGACAGGCAGGATGGGTACGTGCTTCAAGAAAGTGGAAAGCCACCCAGTTGTCACATCTCAGGTGCTGG
ATTTTCTTACACACATGACAGTAGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGAAAGCTGC
CACAGATCTGTTCTCGTTGGGATCCACAGGCCCTATGTATTGAAAGGAAATGTGATGGCTCAG
TCCTTGTAAACATATCATAAGGTTGCACTGACCCAAAGAACAGTTTAATGGACCACTATGAGCCAGTT
CATAAAGAAAAGGAGTGCCTACCCATGTTCTCATCCTCAGAAGAACCTGCCAACGGAGCTCAGTAATATAC
GTGGCCTTCACATGTGAGGAAGCTACTAACACTAGTTACTCTCACAAATGAAGGACCTGGAATGAAAATCTGTG
TCTAAACAAGTCTCTTAAAGTTAGTTAGTGCACATCCAGGCCAGCGCTGGTGCCTCGAGTAATTCTTCTG
TACCTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTCAGCC
AAGAGCCTTTATTGAAAGCTCATCTTCCCAAGACTTGGACTCTGGGTAGAGGAAGATGGAAAGAACAG
AGATTTCAGGAAGAAAATCACATTGTACCTTAAACAGACTTTAGAAAATACAGGACTCCAAATTTCAGTC
TTATGACTGGACACATGACTGAATGAGACCAAAGGAAAGCTTAAACATACTACCTCAAGTGAACCTTATT
AAAGAGAGAGAATCTTATGTTAAATGGAGTTATGAAATTAAAGGATAAAATGTTATTATACAGAT
GAACCAAAATTACAAAAAGTTATGAAAATTAAACTGGGAATGATGCTCATATAAGAACACCTTTAAACTA
TTTTTAACCTTGTGTTATGAAAAAGTATCTACGTTAAATGATATAATCATGATTATTTATGTT
TTATAATGCCAGATTCTTTATGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGACCATT
TTAAATAGAAGTTACTTCATTATATTGACATTATTAATAAAATGTGCAATTGAA

FIGURE 102

MVDVLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQLSLREVKLNNNELETIPNLGPVSANITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGYFDNLANTLLVLKLNRRNRIASAIPPKMFKLPQLQHLELRNKIKNVDGLTFQGLGALKSLKMQRNGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLGYLLMLQELHLSQNAINRISPDAWEFCQKLSLEDDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDLKNNIESWTIEDMNGAFSGLDKLRRRILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMKKLQQLHLNTSSLLCDCQLKWLPQWVAENNQSFVNASCAPQLLKGRSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEMENYAHLRAQGGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTNVNMLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCATAQNSAGSISANATLTVLETPSFLRPLLDRTVKGETAVLQCIAGGSPPPKNWTKDDSPLVTERHFFAAGNQLLIIVDSDVSDAGKYTCEMSNTLGERGNVRLSVIPTPTCDSPQMTAPSLLDDGWWATVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSQGTLADRQDGYSSESSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMLKGKGVYGSDPFETYHTGCSPDPRTVLMHYEPSYIKKKECYPCHPSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459, 628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268, 314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653, 671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962, 1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534, 612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGGCTTGCAAAATG
AAGGATGCAGGACGCAGCTTCCTCTGGAACCGAACGCAATGGATAAAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTCTTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA
TAAACCAGAGTAGACCCGGGGGTGGTGTGTTCTGACATAAATAATCTTAAAGCAGCTGTTCCCCCTCC
CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCAAAGAAAAAGTATGTTCTTCTC
TATAAAGGAGAAAGTGGAGGAGATATTTGGAATGAAAAGTTGGGCTTTTAGTAAAGTAAGAAGACT
GGTGGTGGTGTGTTCTTCTTGTGAAATTCCCACAAGAGGAGAGGAAATTAATAACATCTGAAAGAAA
TTTCAGAGAAGAAAAGTGGACCGCGCAGATTGAGGCATTGATTGGGGAGAGAACCGAGCAGAGCACAGTTGGA
TTTGTGCCATGTTGACTAAAATGACGGATAATTGCAAGTGGATTTCATCAACCTCCTTTTTAAAT
TTTTATCCTTGTGATCAAGATCATGCGTTCTTCTTGTCTTAACACCTGGATTTCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAACGTGTTGAATTCCAGAACGGACCAACACCAGATAAATTATGAATGTTGAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGACCCCTGCTTGTGGTCT
GCTGGCTCTTCAACTCTGTGGTGGCTGGCTGGTGGGGCTCAGACCTGCCCTCTGTGCTCCTGCAGCAA
CCAGTTCAAGGTGATTGTGTTGGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCACCAACACACGGCT
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTCAAGCAGTGGGACTTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACCATGAAATTGGGGCTTCAATGGCTGGCGAACCTCAACACTCTGGA
ACTCTTGACAATGCTTACTACCATCCGAATGGAGCTTGTATACTTGTCTAAACTGAAGGAGCTCTGTT
GCGAAACAACCCATTGAAAGCATCCCTTCTTATGCTTTAACAGAATTCTCTTGCGCCGACTAGACTTAGG
GGAATTGAAAAGACTTCATACATCTCAGAAGGTGCCTTGAAGGTCTGTCCAACCTGAGGTATTGAAACCTTGC
CATGTGCAACCTCGGGAAATCCCTAACCTCACCCGCTCATAAAACTAGATGAGCTGGATCTTCTGGGAATCA
TTTATCTGCCATCAGGCCTGGCTTTCCAGGGTTGATGCACCTCAAAACTGTGGATGATACAGTCCCAGAT
TCAAGTGATTGAAACGGAATGCCTTGACAACCTTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAAC
ATTACTGCCTCATGACCTCTTCACTCCCTGCATCATCTAGAGCGATACATTACATCACACCCCTGGAACTG
TAACGTGACATACTGTGGCTCAGCTGGGATAAAAGACATGGCCCCCTGAAACACAGCTGTTGTGCCGGTG
TAACACTCCCTCCAACTCTAAAGGGGAGGTACATTGGAGAGCTGACCAGAAATTACTTCACATGCTATGCTCCGGT
GATTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAGGCATGGCAGCTGAGCTGAAATGTCGGGCTCCACATC
CCTGACATCTGTATCTGGATTACTCCAAATGGAACAGTCAGTGCACACATGGGGCGTACAAAGTGCAGGATAGCTGT
GCTCAGTGTGATGGTACGTTAAATTCAAAATGTAACTGTGCAAGATACAGGCATGTACACATGTATGGTGGTAA
TTCCGGTTGGGAATACTACTGCTTCAGCCACCTGAAATGTTACTGCAGCAACCACACTCTTCTTACTTTTCA
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGACCGGACCAAGATAACAAATGTGGGCTCCACTCC
AGTGGTCAGTGGAGACCAATGTGACCACCTCTCACACCAACAGAGCACAGGGCGACAGAGAAAAACCTT
CACCATCCCAGTGACTIONTAAACAGTGGATCCCAGGAATTGATGAGGTCTGAAGACTACAAAAATCATCAT
TGGGTGTTTGTGCCATCACACTCATGGCTGAGTGTGCTGGTCTTCAAGATGAGGAAGCAGCACCA
TCGGCAAAACCATCACGCCAACAGGACTGTTGAAATTATTAAATGTGGATGAGATTACGGGAGACACACC
CATGGAAAGCCACCTGCCATGCCTGCTATCGAGCATGAGCACCTAAATCAACTATACAAATCTCCCTT
CAACCACACAACAGTTAACACAATAATTCAATACACAGTTCAGTGCATGAACCGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTACAGAGTTACAAAAAAACAAACAAATCAAAAAAA
GACAGTTATTAAAAATGACACAAATGACTGGCTAAATCTACTGTTCAAAAAGTGTCTTACAAAAAAACAA
AAAAGAAAAGAAATTATTAAAGCTATTGTGATCTAAAGCAGACAAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIIVKNSFKHLRHEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDDELDSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNADFNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWCNCDSL
WLSWWIKDMAPSNTACCACRNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNVGN
TTASATLNVTAATTPFSYFSTVTETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDDIEITGDTPMESHLPMPAIEHEHLNHNSYKSPFNHTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTCGGTTCCCTCTGCTGTTGGGGCA
TGAAAGGGCTTCGCCGGGAGTAAAAGAAGGAATTGACCGGGCAGCGCAGGGAGGAGCGCAGCGACCGC
GAGGGGGCGTGCACCTCGCTGGAGTTGTGCCGGGCCCCGAGCGCGCCGGCTGGAGCTGGTAGCTGGTAGA
GACCTAGGCCGCTGGACCAGGATGAGCGCGCCAGCCTCCGTGCGCGCCGGGGTTGGGCTGCTGCTG
GCGGTGCTGGGGCGCTGCCGGTCCAGCGGGCGTGGAGACTCGGGCAGCCCTCTGGGTAGCGGCC
GAGCGCCCATGCCCAACTACCTGCCGCTGCCCTGGGACCTGCTGGACTGCACTGTAAGCGGCTAGCGCT
CCCAGGCCACTCCGCTGGCTGGACTTAAGTCACAACAGATTATCTTCATCAAGGCAAGTTC
ATGAGCCACCTCAAAGCCTCGAGAAGTGAACACAATGAATTGGAGACCATTCAAATCTGGGACCA
GTCTCGGCAAATATTACACTCTCTGGCTGGAAACAGGATTGTAAGATACTCCCTGAACATCTGAAAGAG
TTTCAGTCCCTGAAACATTGGACCTAGCAGCAACAATTTCAGAGCTCCAAACTGCATTCCAGCCCTACAG
CTCAAATATCTGATCTCACAGAACCGAGTCACATCAATGAACTGGTATTTGACAATTGGCCAACACA
CTCCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCAAAGATGTTAAACTGCCCAACTGCAA
CATCTGAAATTGAAACGAAACAAGATAAAAATGTAGATGGACTGACATTCCAAGGCCTGGTCTGAAAGTCT
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGCTGAGCAACATGAAATTGG
CAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTGCTGATGCTGAGGAACCTCAT
CTCAGCCAAATGCCATCACACAGGATCAGCCCTGATGCCCTGGAGTCTGCCAGAAGCTCAGTGAGCTGGACCTA
ACTTTCAATCATTCAAGGTTAGATGATTCAAGCTTCTGGCTTAAGCTACTAAATACACTGCACATTGGG
AAACAACAGAGTCAGCTACATTGCTGATTGTGCCCTCCGGGGCTTCCAGTTAAAGACTTTGGATCTGAAAGAAC
AATGAAATTCTGGACTATTGAAGACATGAATGGCTTCTCTGGGCTTGACAAACTGAGGCGACTGATACTC
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTCACTGGTTGGATGCACTGGAGCATCTAGACCTGAGT
GACAACGCAATCATGCTTACAAGGCAATGCAATTTCACAAATGAAAGAAACTGCAACAAATTGCAATTAAATACA
TCAAGGCTTTGTGCGATTGCCAGCTAAATGGCTCCCACAGTGGTGGCGGAAACAAACTTCCAGAGCTTGT
AATGCCAGTTGTGCCATCCTCAGCTCTAAAGGAAGAACGATTGCTGTTAGCCAGATGGCTTGT
GATGATTTCCTAAACCCAGATCACGGTTCAGGGAGAACACAGTCGGCAATAAAAGGTTCAATTGAGTT
ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCATGACTTTGCTGGAAAAAGACAATGAACACTGCATGAT
GCTGAAATGGAAAATTATGCACACCTCCGGGCCAAGGTGGAGGTGATGGAGTATACCCATCCTTCGGCT
CGCGAGGTGGAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCAATCAGTTGGTCACTCCTACTCTGTC
AAAGCCAAGCTTACAGTAAATATGCTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGCC
ATGGCACGCTGGAGTGTGCTGCTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGCACAGAC
TTCCAGCTGCACGGAGAGACGCATGTGATGCCAGGGATGACGTGTTTATCGGATGTGAAGATA
GAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTCAGCAAATGCAACTCTGACTGTC
CTAGAACACCATCATTTCGCGCCACTGTTGACCGAATGTAACCAAGGGAGAACAGCCGCTTACAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGTAACCGAGAGGCAC
TTTTTGAGCAGGCAATCAGCTGATTATTGAGACTCAGATGTCAGTGATGCTGGAAATACACATGTGAG
ATGTCTAACACCCCTGGCACTGAGAGAGGAAACGTGCGCTCAGTGTGATCCCCACTCAACCTGCACCTCC
CAGATGACAGCCCATCGTAGACGATGACGGATGGGCCACTGTGGGTGCTGATCATAGCCGTGGTTGCTGT
GTGGTGGGACCGTCACTCGTGGGTGGTCACTCATATACACACACAAGCGGAGGAATGAAGATTGAGCATTAC
AACACAGATGAGACCAACTTGCAGCAGATATTCTAGTATTGTCATCTCAGGGAACGTTAGCTGACAGGAG
GATGGGTACGTGCTTCAAGAAAGGCAACCCAGTTGTCACATCTTCAGGTGCTGGATTTCCTTACCA
CAACATGACAGCTAGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTTGGAAGCTGCCACAGATCTGTT
CTTTGCTCGTTGGATCCACAGGCCCTATGTTAGGAAAGGAAATGTCATGGCTCAGATCCTTTGAAACAA
TATCATACAGGTTGAGCTCTGACCCAGAACAGTTAAAGGACCATATGAGCCCAGTTACATAAAGAAAAG
GAGTGTACCCATGTTCTCATCTTCAGAAGAATCCTGCAACGGAGCTCAGTAATATATCGTGGCTTCCACAT
GTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAAGGACCTGGAAATGAAAATCTGTTCTAAACAGTCC
TCTTTAGATTAGTGCACCCAGAGCCAGCGTGGCTCGAGTAATTCTTCAGTGGTACCTTGGAAA
GCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATGTCAGCCAAAGGCCCTT
TTGAAAGCTCATTCTCCAGACTTGGACTCTGGTCAAGAGGAGATGGAAAGGAAAGGACAGATTTCAGGAA
GAAAATCACATTGTACCTTAAACAGACTTAAAGGAAACTACAGGACTCCAAATTTCAGTCTTATGACTTGGAC
ACATAGACTGAATGAGACCAAAGGAAAGCTTAAACATACTACCTCAAGTGAACCTTATTAAAGAGAGGAAT
CTTATGTTTAAATGGAGTTATGAAATTAAAAGGATAAAAGTGTATTATTAACAGATGAACCAAATTAC
AAAAAGTTATGAAAATTATGAGGAAATGATGCTCATATAAGAAATACCTTTAAACTATTGAAACTTGT
TTTATGCAAAAAGTATCTACGTAATTAAATGATATAAAATCATGATTATTGTTATGTTATGACTTGGAC
TTTCTTTTATGGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCATTTAAATAGAAGTT
ACTTCATTATATTGACATTATTTAAATAAAAGTGTCAATTGAAAAAAAAAAAAAAAAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQLSREVKLNNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRIASIAPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMGAFWGGLSNMEILQLDHNNLTEITKGWLGYGLLMLQELHLSQNAINRISPDAWEFC
QKLSLEDDLTNFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLGSSLKTLDDLKNNEIS
WTIEDMNGAFSGLDKLRRLILQGNRIRSIKKAKFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQLQHLNTSSLLCDCQLKWLPPQWAENNFQSFVNASCAPQLLKGRSIFAVSPDGFCVDDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEMENYAHLRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPPAQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLRTVKGETAVLQCIAGGSPPPKNWTKDDSPVVTERHF
FAAGNQLLIIVDSDVSDAGKYTCMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLLDDGWA
TVGVVIIAVVCCVVGTSLVWWVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTLADRQ
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLCPLGSTGPMY
LKGNVYGSDPFETYHTGSPDPRTVLMHDYEPSYIKKKECYPCHPSEESCRFSNISWPS
HVRKLLNTSYSNEPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTCGGGAGAGGCCAGCTTGACTTGAAATGGAAGGAGCCCAGGCCGGAGCGCAGCTGAGAC
TGGGGGAGCGCTTCGGCTGTGGGGCGCCGCTCGGCCGGGGCCAGCAGGAAAGGGAAAGCTGTGGTCTGCC
CTGCTCCACGAGGCGCCACTGGTGTGAAACGGGAGAGGCCCTGGTGGTCCCGTCCCTATCCCTCTTTATATA
GAAACCTTCCACACTGGAAAGGCAGCGCGAGGAGGGCTCATGGTGAGCAAGGAGGCCGCTGATCTGAG
GCGCACAGCATTGGAGTTACAGATTTACAGATACCAAATGGAAGGCGAGGAGGCAGAACAGCCTGCCTGGT
TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCAGAGGCCGGTGCTGC
TGCTCCTGCTGCTGCTGCCACAGCTGCACCTGGGACCTGTGCTTGCCTGAGGGGCCAGGATTGGCCGAA
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTGCGGAGGAGGCCGTGCTGGTACTGAGGCCCTGAGG
AGCCCCGGCTGGCCAGCCGGTCAAGCTGCCCGAGACTGTGCCCTGTTCCAGGAGGGCGTGGACTGTG
GCGGATTGGACCTGCGTGAGTCCCCGGGACCTGCCCTGAGCACCCAACCSTATCTCTGCAGAACACCAGC
TGGAAAAGATCTACCCCTGAGGAGCTCTCCCGCTGCACCCGGCTGGAGAACACTGAAACCTGAAAACAAACGCC
CTTCCCAGGGCTCCAGAGAACGGCTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAAACAGC
TGACCTTGGCACCCCGTCTCTGCAAAACGCCCTGATCAGTGTGACTTGTCTGCCAACTATCTACCAAGATCT
ATGGGCTCACCTTGGCCAGAACGCAAACCTGAGGTCTGTGACTCTGCACAAACAAGCTGGCAGACGCCGGC
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTGAGGTCTCATCTGTCCAGCAACTTCTGCCACGTG
CCAAGCACCTGCCCTGCCCTGTAAGCTGCACCTCAAGAACAAAGCTGGAGAACATCCCCCGGGGCG
TCAGCGAGCTGAGCAGCCTGCGAGCTATACTGCAGAACAAACTACCTGACTGACGAGGGCTGGACAACGAGA
CCTCTGGAAGCTCTCAGCCTGGAGTACCTGGATCTGTCAGCAACACCTGTCTGGTCCAGCTGGCTGC
CGCGCAGCCTGGTCTGCTGCACCTGGAGAACGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCCATCC
GCAGCCTGGAGTACCTGCTGCTGCACAGCAACCAGCTGCCAGGAGCAGGGCATCCACCCACTGGCCTCCAGGGC
TCAAGCGGTTGACACGGTGCACCTGTACAACAAACAGCGCTGGAGCGCTGCCAGTGGCTGCCCTGCC
GCACCCCTCATGATCCTGCACAACCAGATCACAGGCATTGGCCGGAAGACTTGCACCCACTACTCCTGGAGG
AGCTCAACCTCAGCTACAACCGCATCACAGCCCACAGGTGCACCGCCTCCGCAAGCTGCCCTGCTGC
GCTCGCTGGACCTGTCGGCAACCGCTGCACACGCTGCCACCTGGCTGCCCTGAAATGTCCATGTGCTGAAGG
TCAAGCGCAATGAGCTGGCTGCCCTGGCACAGGGGGCGCTGGCGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA
CCAGCAACCGACTGCGCAGCCCTGGGCCCGTGCCTGGTGGACCTGCCCATCTGCAGCTGCTGGACA
TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGCTCCCGAGTCAGTGTACCTGAGAACAAACA
AGATTAGTGCCTGGCCCGCCAATGCTTCGACTCCACGCCAACCTCAAGGGGATCTTCTCAGGTTAACAAAGC
TGGCTGTGGCTCCCGTGGAGCAGTGCCTCCGGAGGCTGAAGCACCTGCAAGGTCTTGACATTGAAGGCAACT
TAGAGTTGGTGCACATTCCAAAGGAGCGTGGCCGTTGGGAAGGAAAAGGAGGAGGAGGAAGAGGAGGAGGAGG
AGGAAGAGGAAACAAAGATAGTGACAAGGTGATGAGATGTGACCTAGGATGATGGACCGGGACTTTCTGC
AGCACACGCCCTGTCGTGAGCCCCCACTCTGCCGTGCTCACACAGAACACCCAGCTGCACACATGAGGCA
TCCCACATGACACGGCTGACACAGTCTCATATCCCCACCCCTCCACGGCGTGCCTCACGGCCAGACACATGC
ACACACATCACACCCCTCAAACACCCAGCTCAGCCACACACAACCTACCCCTCAAACACCACAGTCTGTACAC
CCCCACTACCGCTGCCACGCCCTGTAATCATGCAGGGAGGGCTGCCCTGCCCTGGCACACACAGGCA
TCCCCTCCCCCTGTCGACATGTGATGCGTATGCATACACACCACACACACATGCACAAGTCATGTGCGAA
CAGCCCTCCAAAGCTATGCCACAGACAGCTTGCCTGCCAGCCAGAATCAGCCATAGCAGCTGCCGTCTGCC
GTCCCATCTGTCGTCCCGTCCCTGGAGAACACACAAGGGTATCCATGCTCTGTCAGGCCAGGTGCC
GGAACTCACAAAAGCTGGTTTATCCTTCCATCCTATGGGGACAGGCCCTCAGGACTGCTGGCCTGGCC
TGGCCACCCCTGCTCCTCCAGGTGCTGGCGAGTCACTCTGCTAAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCACCTTCCAATGGGCAAGCCCAGTGGAGGAGGAGGCCCTGGGTGCTGCTGGGGCCTTGGGG
CAGGAGTGAAGCAGAGGTGATGGGGCTGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTT
GTTCTCAGGCCTGTGGGGAAAGTCCGGGTGCTTTATTTTATCTTCTAAGGAAAAAAATGATAAAAAT
CTCAAAGCTGATTTTCTTGTATAGAAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAAA

FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENFAEEEPLVLSPEEPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSDANVLPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPDRVTLMILHNQITGIGREDFATTYF
LEELNLSYNRITSQPVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKIGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCGCGCCTGCCGCTGCTCTCCGGGAGCGGCAG
CACTAGCCGGCGCGAGGGCTGGGGTTCTCGAGACTCTCAGAGGGCGCCTCCATGGCCCACCA
CAACCTGTTCTCGCGCCACTGCCTGCCAGGACCCGCTGCCAACATGGATTTCCTGGCGCTGGT
GCTGGTATCCTCGCTCACCTGCAGGCGGCCGAGTCAGCGGAGGTGGCCAGGAAATAGTGTATCGAT
TGGCTATGCTTATGGGGAGGATTGACTGCTGCTGGGGCTGGCTGCCAGTCTGGGACAGTGTAGCC
TGTGCCAACCACGATGCAAACATGGTGAATGTATGGGCAAACAAGTGAAGTGTATCCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGCCCTGTAAGCACAGGTGATGAACACTTA
CGGCAGCTACAAGTCTACTGCTCACCGATAATGCTCATGCCGATGGTCTCTGCTCAAGTGCCCTGACCTG
CTCCATGGCAAACGATGCTAGTGGCTGTGATGTTAAGGACAAATACGGTGCAGTGCCATCCCTGGCCT
GCACCTGGCTCTGATGGGAGGACCTGTGAGATGTTGATGAATGTGCTACAGGAAGGCTCCTGCCCTAGATT
TAGGCAATGTCACACTTGGGAGCTACATGCTCAAGTGTGATGCTAAAGGCTTCGATCTCATGTATATTGGAGG
CAAATATCAATGTCATGACATGACAAAGCAATGCTCACTGGTCAAGTGTGCTGGCAGCTTGCTCGATGTTAA
CGTACGTGGTCTACAAGTGCRAAATGTAAGGAGGATACCAAGGGTGAATGGACTGACTTGTGTTATATCCAAA
AGTTATGATTGAAACCTTCAGGTCATTGATACAGGAAATGGTACCTTAAAGGGTGAACACAGGAAA
TAATAATTGGATTCTGATGTTGAGTACTTGGCTCCGAAGACACCATATATTCCCTATCATTACCAA
CAGGCCTACTCTAACGCAACACAAGACCTACACCAAGCCAACACCAATTCTACTCCACCACCA
CCTGCCAACAGAGCTCAGAACACCTTACACCACTACACCCAGAAAGGCCAACCAAGGGACTGACA
ACTACAGGCTGCACTACACCCAGGGATTACAGTTGACAACAGGGTACAGACAGACCCCTGAGAAACCCAGG
AGATGTGTCAGTGTCTGGTACACAGTGTAAATTGACCATGGACTTTGGATGGATCAGGGAGAAAGACAA
TGACTTGCACTGGAACCAATCAGGGACCCAGCAGGTGACAATATCTGACAGTGTGGCAGCAAAGCCCCAGG
GGGAAAAGCTGCACGCTGGTGTACCTCTGGCCCTCATGCATTGAGGGACCTGTGCTGTGATTAGCA
CAAGGTGACGGGCTGCACTCTGGCACACTCCAGGTGTTGTGAGAAAACACGGTCCACGGAGCAGCCCTGTG
GGGAAGAAATGGTGGCCATGGCTGGAGGCAAACACAGATCACCTTGCAGGGCTGACATCAAGAGCGAATCACA
AAGATGATTAAGGGTTGAAAAAAAGATCTATGATGGAAATTAAAGGAACTGGATTATTGAGCCTGGAGAAG
AGAAGACTGAGGGCAAACCAATTGATGGTTTCAAGTATATGAAGGGTGGCACAGAGAGGGTGGCACCAGCTG
TTCTCCATATGCACTAAGAATAGAACAGAGGAAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTGGCAGG
GCCATTGTTAGAATACTTCATAAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTCTTCTAAATTAGA
AAAAATTGCTTATTAAGATGGTTAAGATGTTCTACCAAGGAAAGTAACAAATTATAGAAATTCCCAA
AGATGTTTGATCCTACTAGTAGTGTGAAATCTTGAAGACTAAATAATTGGACAAGGCTTAATTAGG
CATTTCCCTTGTGACCTCTAATGGAGAGGGATTGAAAGGGAAAGAGGCCACAAATGCTGAGCTCACTGAAATA
TCTCTCCCTTATGGCAATCTAGCAGTATTAAGAAAAAAAGGAAACTATTATTCCTAAATGAGAGTATGATGGAC
AGATATTGTTAGTATCTCAGTAATGCTCTAGTGTGGCGGTGGTTCAATGTTCTCATGGTAAAGGTATAAGCC
TTTCATTGTCATGGATGATGTTCAAGATTGTTCTTAAGAGATCCTCAAGGAACACAGTTCAGAGAG
ATTTTCATGGGTGCATTCTCTCGCTCGTGTGACAAGTTATCTGGCTGCTGAGAAAGAGTGCCCTGGCCCC
ACACCGCAGACCTTCCCTCACCTCATCAGTATGATTGATTGCTCTCTTATCAATTGGACTCTCCAGGTTCCAC
AGAACAGTAATATTTTGAAACAATAGGTACAATAGAAGGTCTCTGTCATTAAACCTGGTAAAGGCAGGGCTGG
AGGGGGAAAATAATCATTAAGCCTTGAGTAACGGCAGAATATGGCTGTAGATCCATTGTTAATGGTTCATT
TCCTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGAAAATAATGAAATTGTTACTTTGATGCCAA
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTTATTATTAATGTTT
CTAAAATAAAATGTTAGTGGTTCCAAATGGCTAATAAAAACAATTGTTAAATAAAACACTGTTAGTAAT

FIGURE 110

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRTCDVDECATGRASCPRFRCQ
VNTFGSYICKCHKGFDLMIYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHPKGNGTILKGDTGNNNWIPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTTPERPTTGLTTIAPAASTPPGGITVDN
RVQTDPQKPRGDVFSQLVHSCNFDHGLCGWIKEKDNDLHWEPIRDPAQQYLTVA
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSCTLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTGCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACTTCCCTTGCAACAGGTGCTGCTCGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTAGGCCCTACCTACCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCA
CACAAATGCCAAATACTTA~~CT~~GGCTGTGAATAAGTCTGTGGTCTGACTTGAATACC
AACACAAGTCACCATGATGCCACCCAA~~T~~GATCTGCTTATCAACCCACTGCAGTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATT~~C~~AGGAAATGGA~~A~~CTCTATCTGCCAGTCA
GAAGATA~~C~~ACAAGTCACGGTTGATGATCCTGTACAAAGCCAGTGGTGCAGATT~~C~~ATCCTCCCT
CTGGGGCTGTGGAGTATGTGGGAACATGACCTGACATGCCATGTGGAAAGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTC
TCCCCAAAACAATACCC~~T~~CATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
GCCTGGTGAGGAACCC~~T~~GTCAGTGAATGGAAAGT~~G~~ATATCATTATGCCATCATATTAT
GGACCTTATGGACT~~T~~CAAGTGAATTCTGATAAAGGGCTAAAGTAGGGGAAGT~~G~~TTTACTGT
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAA~~G~~CATGGGCCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGGCCAGAAGACAATGGACTATGTGTGCTGCTTACAACAACATAAC
CGGCAGGCAAGATGAAACTCATTCACAGTTATCATCACTCCGTAGGACTGGAGAAGCTG
CACAGAAAGGAAAATCATTGTCACCTTAGCAAGTATACTGGAA~~T~~ATCACTATT~~T~~TGATT
ATATCCATGTGCTTCTCTTCCATGGAAAAAATATCAACC~~T~~ACAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAACAGAATACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTCGAATATATGAATTGTTGCTTCCAGATGTTCTGGT~~G~~TTCCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTG~~T~~TGATCGGGCAAGATTGCACAGTACAGT
GTATGAAGTTATT~~C~~AGCACATCCCTGCCAGCAGCAAGACC~~A~~CCATCCAGAGT**GA**ACTTT~~C~~ATGG
GCTAACAGTACATTGAGTGAAATTCTGAAGAAA~~C~~ATT~~T~~TAAGGAAAACAGTGGAAAAGT
ATATTAA~~T~~CTGGAATCAGTGAAGAAACCAGGACCAACACCTCTACTCATTATT~~C~~TTACA
TGCAGAATAGAGGCATTATGCAAATTGA~~A~~CTGCAGGTTT~~C~~AGCATATACACAATGT~~C~~TT
GTGCAACAGAAAACATGTTGGGAA~~A~~ATT~~C~~CTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGTT~~C~~CTCATAAGTTTGATGAA~~A~~ATCTACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGCTCACCTACAAA
TGTGGAAACTTTACATTGTTG~~C~~ATT~~T~~TCAGCAGACTT~~G~~TTTATTAAATT~~T~~TATTAGTG
TTAAGAATGCTAAATT~~T~~TGTTCAATT~~T~~TATT~~C~~AAATT~~T~~CTATCTGTTATTGTACAA
CAAAGTAATAAGGATGGTTGT~~C~~ACAAAAA~~C~~AAACTATGCCTCTCTTTTTCAATCACC
AGTAGTATT~~T~~TGAGAAGACTGTGAACACTTAAGGAAATGACTATTAAAGT~~C~~TTATT~~T~~TA
TTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTTGT~~T~~TTAAAAA~~A~~AAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGTLSASQ
KIQVTVDPPVTKPVVQIHPPSGAVEYVGNMTLTCHEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEVAFPDVSGVSRIPSRSVPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTGCAGTTCCCCTGGCAGTCCTGGTGTGCTGTT
GCTTTGGGGTGCTCCCTGGACGCACGGGCGGAGCAACGTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTATGCCCGTGGTGCCTGCT
TGTCAAAATCTCAACCGGAATGGGAAAGTTGCTGAATGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCTACTATTATCATTGTAAGATGGTGAATTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAAACTTATAAGTATAAGAGTGGAAAGAGTATTGAGGCCGTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTATTGAAGACCTGGATTGCCAGTGTGGGATCATATACT
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC
AGATTGCCTTGTCCCTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTCAAAAAAAT
TATTATCAGAATCTGCACAACCTTGAAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGC
CATAAAGACAACGCTCTGGTCCATCATTGCCACAGATAAACTAGTTAAATTTATAG
TTATCTTAATATTATGATTTGATAAAACAGAAGATTGATCATTGTTGGTTGAAGTG
AACTGTGACTTTTGAAATTGCAGGGTTCAGTCTAGATTGTCATTAAATTGAAGAGTCTA
CATTCAGAACATAAAGCACTAGGTATACAAGTTGAAATATGATTTAAGCACAGTATGATG
GTTTAAATAGTTCTAATTTGAAAAATCGTGCAAGCAATAAGATTATGATATTGTT
TTAATAATAACCTATTCAAGTCTGAGTTGAAAATTACTTCCCAAGTATTGCATT
TGAGGTATTTAAGAAGATTTTTAGAGAAAATTTCTCATTTGATATATTTTCTCTG
TTTCACTGTGAAAAAAAGAAGAATTTCCATAAATGGGAAGTTGCCATTGTCTCAAG
AAATGTGATTTCAGTGACAATTCGGGTTTTAGAGGTATTCCAAATTCCTG
ATTTTTAGGTTATGCAACTACTTACTTAAAGTTCAGGTATTCTCTGTGATTC
TGGTAATACAGGATGTACTGATTTAGAGTTTTAAAGTTCAGGTATTCTCTGTGATTC
CAACAAAGTTGATTCTCTGTATTTCTACTTAATGGGTACTTTTATTT
CAAATGGATGATATTCTGGAAACATTTTTATGTTTAGAAACAGTATTTTTGT
GTTCAAACTGAAGTTACTGAGAGATCCCATCAAATGAACAATCTGTGTTAATTTAAATT
TTGGCCACTTTTTCAGATTTACATCATTCTGTGAACTTCAACTGGAAATGTTTT
TTCTTTTTGGATGTGAAGGTGAACATCCCTGTATTTGTCTGTGTAAAAGCCTGGTA
TTTTACATTTTGAAAATTCAAAGCTTAATTAAAAGTTGTCATTCTACTCAGGAAAAG
CACTCTGTTAATGTCTTAATGTATTTCTGTCCTCATACAGGAAATGTCTTAATGTAT
TTTACAGTCTGTTAATGTCTGTATTTAAATAAACATTTTTATTTTTAAAGACAA
ACTTCAATTTATCCCTGTGTTTCTCTGTACTGGTAATTTGTGTGGATTTCACGGTAA
GTCAGTAGGTGGAAACATTTTAGTGTATTTTTACTCCTAAAGAGGTCAGAATACATAGTT
CACTTTAAAGGGGGAAATCAAAATACAAGTGAATCAACGTACCACCATTACGTAGTAGA
AATTCTGTTAATGTCCCTCTTAGGCTGTGTGTGAATCCCATTGAATTTACAG
TACGTAATTACAAGTTCTTTAAAGCCCTCTCTTAGAATTTAAATTTGTACCA
AAAGATTTGGATGTGTTACTGTGTATGCCTTAGAAAAAATTCTAAGCAAAAAACCT
TTCTTAACCACTCATTAAAGGTGAAAAAAAAAAAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPYPSKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNPAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCGAGTGTCCAGCTGGGAGACCGTGATAATTGTTAACTAATTCAACAAACGGGACCCTT
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGACAGGCAGGATTGGAAGAGCGGG
AAGGTCTGGCCCAGAGCAGTGTGACACTTCCTCTGTGACCATGAAACTCTGGGTGTCTGC
ATTGCTGATGGCTGGTTGGTGTCTGAGCTGTGAGGCGAATTCTCACCTCTATTG
GGCACATGACTGACCTGATTATGAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGCAACAAAATGGAAGCCTTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG
TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTGCTCTGCAGGACTCAGCTGCA
GGTTTATGCCAACCTCTGTGAGCGGCAGTTCTCCCCACTGATGAGGACGGAGATAAGG
AGCTGCCAACGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA
GAGGGGAACCTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG
GGCCGCTCGGCCTACAATGAAGGGACTATTATCATACTGGTGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGGAGGGAGGCCACCAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGCTTCCAGTTGGGTGATCTGACCGTGCCTGGAGCTCACCGCCGCCTGCTC
TCCCTGACCAAGCCACGAACGAGCTGGAGGAACTGCGGTACTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAGGCA
TCTATGAGAGGCCTGGACTACCTGCTGAGAGGGATGTTACGAGAGCCTGTCGTGG
GAGGGTGTCAAACGTACACCCCCTAGACAGAAGAGGCTTCTGTAGGTACCAACATGGCAA
CAGGGCCCCACAGCTGCTATTGCCCTTCAAAGAGGAGGACGAGTGGACAGCCGCACA
TCGTCAGGTACTACGATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
CCTAAACTGCACGAGCCACCGTTGATCCAAAGACAGGAGTCCTACTGTCGCCAGCTA
CCGGTTTCCAAAGCTCTGGCTAGAGGAAGATGATGACCTGTTGTGGCCCGAGTAAATC
GTCGGATGCAGCATATCACAGGGTAACAGTAAAGACTGCGAGATTGTTACAGGTTGCAAAT
TATGGAGTGGAGGACAGTATGAACCGCACTTCGACTTCTAGGCGACCTTTGACAGCGG
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTGCGGAGCGGGAAAGGTGACTACCGAACAGACATGCTGCTGCC
TGTGCTTGTGGCTGCAAGTGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT
TGAGACCTTGTGGATCAACAGAAGTTGACTTGACCATCCTTCTGTGCTTCCCTGGTC
CTTCAGCCCATGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGGACTCCTGT
GTGACTGAAGTCCCAGCCCTTCCATTAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCAAGTGAACCAAAGTTCTGATACCTTGTACATGTTGTTTAT
GGCATTCTATCTATTGGCTTACAAAAAATAAAATGTCCCTACCAGAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGDYYHTV
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
YFEQLLEEREKTLTNQTEALATPEGIYERPVVDYLPERDVYESLCRGEVKLTPRRQKRLF
CRYHHGNRAPQLLIAPKEEDEWDSPHIYRYYDVMDSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPLGAAIWPKKGTAVFWYNLLRSGEDYR
TRHAACPVLVGCKWVSNKFHERGQEFLRPCGSTEV

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTCCTCTTTAGTGGAAAGACAGACCCATAATCCCAGTGTGAGTGAAATTGATTGT
TTCATTTATTACCGTTGGCTGGGGTTAGTTCCGACACCTTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA
AGACAGGACAATCTTCTTGGGATGCTGGTCTGGAAAGCCAGCGGGCCTGCTCTGCTCTTGGCCTCATTGACCC
CAGGTCTCTGGTAAAACCTGAAAGCCTACTACTGGCCTGGTCCCCATCAATCATTGATCCTTGAGGCTGTGCC
CCTGGGCACCCACCTGGCAGGGCTACCACCATTCGACTGAGCTCCCTGTTGGCTCTGCTGCCAGCGCTTC
CCCTCATCTTAGGGCTGTCCTGGGGTGCAGCCTGAGCCTCTGCGGGTTCTGGATCCAGGGGAGGGAGAAC
ATCCCTGTGTGAGGCTGTAGGGGAGCGAGGAGGGCACAGAACATCCAGATTGAGAGCTCGGCTAGACCAAAGTG
ATGAAGACTTCAAACCCGGATTGTCCCCTACTACAGGGACCCAAACAAGCCTACAAGAAGGTGTCAGGACTC
GGTACATCCAGACAGAGCTGGGCTCCGTGAGCGGTTGTCGGTGGCTGACCTCCGAGCTACACTGTCCA
CTTTGGCCGTGCTGTGAACCGTACCGTGGCCCATCACTTCCCTCGGTACTCTACTTCACTGGCAGCGGGGG
CCCAGGCTCCAGCAGGGATGCAAGGGTGTCTCATGGGATGAGCGGCCGCTGGCTCATGTCAGAGACCCCTGC
GCCACCTTACACACACTTGGGGCCACTACGACTGGTTCTTCATCATGCAAGGATGACACATATGTGCAGGCC
CCCCCTGGCAGCCCTGCTGGCCACCTCAGCATCAACCAAGACCTGACTTAGGCCGGCAGAGGAGTTCATTG
GCGCAGCGAGCAGGGCCGTACTGTCACTGGGCTTGGCTACCTGTCACGGAGTCTCTGCTTCGTC
GGCCACATCTGGATGGCTGCCAGGGAGACATTCTCAGTCCCCTGTCAGGAGTGGCTGGACGCTGCCCATTG
ACTCTCTGGCGCTGGCTGTCTCACAGCACAGGGCAGCAGTATGCTCATTTGAACATGGCCAAAAAATAGGG
ACCCGTAGAAGGAAGGGAGCTCGGCTTCTGAGTGCCTTCGCGTGCACCCCTGCTCCGAAGGTACCCCTATGT
ACCGCTCCACAAACGCTCAGCCTCTGGAGTTGGAGCGGGCTTACAGTGAATAGAACAACTGCAGGCTCAGA
TCCGGAACCTGACCGTGTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCGTTGGCTCCCTGCTCCTTCA
CACCAACACTCTGCTTGGAGGTGCTGGCTGGACTACTTCACAGAGCAGCACACCTCTCCTGTCAGATGGGG
CTCCCAAGTCCCACACAGGGGCTAGCAGGGCGAGTGGTGTGCTGGAGACTGCCCTGGAGCAGCTCA
ATCGCGCTATCAGCCCCCCTGCGCTTCCAGAACAGCAGCGACTGCTCAACGGCTATCGGGCTTCGACCCAGCAC
GGGGCATGGAGTACACCTGGACCTGCTGTGGAATGTGTGACACAGCGTGGCACCGGGGGCCCTGGCTCGCA
GGGTCACTGCTGCCACTGAGCCGGGTGAAATCTACCTATGCCCTATGTCACTGAGGCCACCCAGTGC
AGCTGGTGTGCCACTCTGGTGGCTGAAGCTGCTGCAGCCCCGGCTTCCTGAGGCGTTGAGCCAATGTCC
TGGAGCCACGAGAACATGCTTACCCCTGTTGCTGGCTACGGGCCACGAGAACGGTGGCGTGGAGCTCCAG
ACCCATTCTGGGTGAAGGCTGCAAGCAGCGAGTTAGAGCAGGGTACCTGGACGAGGCTGGCCTGGCTCG
CTGTGCGAGCAGAGGCCCTTCCAGGTGCACTCATGGACGTGGCTCGAAGAACAGCACCCTGAGGACTCTCT
TCTTCTTACCAACCGTGTGGACAAGGCTGGCCGAAGTCTCAACCGCTGTCATGAATGCCATCTGGCT
GGCAGGCCAGGAAGAGGGAGGAAGGCCCTGGAGGGCTGGAGGGTGTGGATGTTCTCCGCTCAGGGCTCC
ACCTCTTCGGCCGTAGAGCCAGGGCTGGTGCAGAACATTCTCCCTGCGAGACTGCAGCCCCAGGCTCAGTGAAG
AACTCTACCAACCGCTGCCCTCAGAACCTGGAGGGCTAGGGGCCGTGCCAGCTGGCTATGGCTCTTTG
AGCAGGAGCAGGCCAATAGCACTTAGCCCCTGGGGCCCTAACCTTACCTTGTCTGCCAGCC
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTAAATATGAAAATGTTATTAA
ACATGTCTTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDNRARLD
QSDEDFKPRIVPYYRDPNKPYKKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQQVSHGDERPAWLMSETLRHLHTFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
DILSARPDEWLGRCLIDS LGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPNSRFEV
LGWDYFTEQHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRYQPRLRFQKQRLLNGYR
RFDPARGMETYTL DLLECVTQRGHRRALARRVSSLRPLS RVEILPMPYVTEATRVQLVLPLL
VAEAAAAPAFLEAFAANVLEPREHALLTLLVYGPREGGRGAPDPFLGVKAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPGPEVLNRCRMNAISGWQAFFP
VHFQEFPALSPQRSPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEAELEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRAGLAMALFEQEANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGC~~CCAACGTGAGAGGAACCGTGCGCGCTGCGCTTCCTGTCCCCAAGCC~~
GTTCTAGACGCCGGAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTTGG
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGGCTGCAGTAAAGGAGACTGGACAAACACTGTGACAAAGCAG
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCAATTATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACAACTG
GTTCTCCTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTAATACCAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC
CAACCAGGTAGTAGAAGGCTGTTGTTAGATATGGCTGTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGTATGGGTATACCGCCTTAGGGCATTTGGCATTTTCAAT
GATGCATTGGTTTCTTACCTCCAAATGGCTGACAATGACTTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACATATCCAA
TACAGCTGTATGTTCTTTCTTCTAATTGGTGGCACTGGTATAACCACACATAAAG
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAAACACATGAACATTGAAATG
TGTTGGAAAGAAGTGTGTTAAGAATAATAATTGCAAATAACTATTAAATAATTATAT
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTGCTGATTGGTT
AAAAAAATTAAACAGGTCTTAGCGTTCTAACAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAAACCTTAGCTGTGTGTTCCCTTACTCTAACACTGATTATGTTCT
AAGCCTCCCCAAGTCCAATGGATTGCCTCTAAAATGTACAACTAAGCAACTAAAGAAA
ATTAAAGTGAAGTGTGAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLLWAAVKETWTKHCDKAEFFSSENVKFESINMDTN
DMWLMMRKAYKYAFDKYRDQYNWFFLARPTTFAIIEENLKYFLLKKDPSQPFYLGH
TIKSGDLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMIWKISED
KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPNQVVEGCCSDMA
VTNFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFLPPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCNYGSGSVKNCCPLNWEYFQSSCYFFSTDТИWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQVDGTPLTKSLSFWDVGEPNNIATLEDCATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCCCGCTGCCGCTGGCCCCCTCAGCAACCCCTGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCCGCTCGGCTGCCTGACTTCTCCTGCTGCTGCTTTCAAGGGGCTGCCTGATAAGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCCAGTGGTACAGGAATTGAAAGTGTGGAACTGTCTTGCACTCATTACGGATTGCG
AGACAAGTGA~~CCC~~CAGGATCGAGTGAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGCTGTGAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTGAGGTCGTTGCTGAAATGACCGCAAGGAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGGCAGGGCTTACAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGCCACCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT
CCAGAGCCAATCCCAGATTGCAATTCTTCTTCCACTTAAACTCTGAAACAGGCACTTGGTGTACTGCTG
TTCACAAGGACGACTCTGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATGGCGAATTATTGGGGGGTTCTGGTTGCTGCTGTACTGGCCCTGA
TCACCTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACCAGATGGAGTTAATCACATCCGCACTGACGAGGGCGACTTCAGACACAAGTCATGTTG
TGATCTGAGACCCCGCGGTGAGGCGACAGAGCGCACGAGCTAGACACTCATTCAGAAGCTTCTGTTGGCCAAAGTTGACCA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTCAGAAGCTTCTGTTGGCCAAAGTTGACCA
CTACTCTTCTTAACAAAGGCCATGAATAGAAATTTCCTCAAGATGGACCCGGTAAATAACCAACAA
CGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCTTAATCTGTTCTGGCTGATTCGGCATGAGTATTAGG
GTGATCTTAAAGAGTTGCTCACGTAACGCCGTGCTGGCCCTGTGAAGCAGCATGTTACCAACTGGTGT
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCGGGGAAACCCA
GAAAAGCTTCTTACACAGCAGCCTTACATCGGCCACAGACACCACCGCAGTTCTTAAAGGCTCTGC
TGATCGGTGTCAGTGTCCATTGGAGAACGTTTTGGATCAGCATTTGTTAAACACCAAAATCAGGAAG
GTAAATTGGTTGCTGGAAGAGGGACTTGCCTGAGGAACCCCTGCTTGTCCAACAGGGTGTCAAGGATTTAAGGAAA
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTCTATGGGTCTGTTATTATAAAATT
TACATCTAAATTGGCTAAGGATGTATTGATTATTGAAAAGAAAATTCTATTAAACTGTAATATATTGT
CATACAATGTTAAATAACCTATTGGGTTAAAGGCTTCAACTTAAGGTAGAAGTCCAAGCTACTAGTGTAAAT
TGGAAAATATCAATAATTAGAGTATTGACCCAGGAATCCTCTCATGGAAGTTACTGTGATGTTCTTCT
CACACAAGTTAGCCTTTTCAAGGGAACTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAATTCCAGTTAACGCAATGTTGAAATCAGTTGCATCTCTCAAAAGAAACCTCTCAGGTTAGCTTGA
GCCTCTCCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCTCAGATGTACATACAGATG
CCAGTCAGCTCTGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTCCTCGCTGCTGCCAGGAGGCC
GCCATCCCTGGGCCCTGGCAGTGGCTGTGCTCCAGTGAGCTTACTCACTGCGCCCTTGCTCATCCAGCACAGC
TCTCAGGTGGGCACTGCAGGGACACTGGGTCTTCCATGTAGCGTCCCAGCTTGGCTCTGTAAACAGACCTCT
TTTGTTATGGATGGCTCACAAATAGGGCCCCAATGCTATTGTTAAAGTGTGTTAATTATTGTT
AAGATGTCAGGCAAAGGCAATTGCGAAATCAACTGTCAGTACAATAACATTAAAAGAAAATGGAT
CCCAGTGTCTCTTGCACAGAAGCACCCAGGCCACAGGCTCTGCGCATTTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAAGGTGGAGCAGCCAGGTGAAAGGCTGGGGAGGAAAG
TGAAAAGCCTGAATCAAAGCAGTTCTAATTGACTTTCAATTGTTACCCAGGAGACACTGCTCC
TGTGGGGGACATTGCAACATCACTCAGAACGCTGTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCC
GCCGTGCTGGACTCAGGACTGAAGTGTGAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCC
GAATGGCTCTCAACTCAGCTGCTTTCACTGCTTCCAGTGTCTGGTTTTTACTTTGACAGCTTT
AATTGCAACATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGCAGGCCAGGGCCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTCTGCTGCATGGCATTGGATGCTAGCATGCAAGTTC
CCTCCATCATTGCCACCTGGTAGAGGAGGGATGGCTCCCCACCCCTAGCGTTGGGATTACGCTCCAGCCTC
TCTTGGTTGTCAGTGATAGGGTAGCCTTATTGCCCTCTTCTTACCCCTAAACCTCTACACTAGTGCCA
TGGGAACCAAGGCTGAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTTAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAAC
CTCATTATAAAAGCTTCAAAAAACCCA

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRRLCARLPDFLFFFRLGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVRRDSALYRCEVVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267